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OM protein - protein search, using sw model

Run on: February 25, 2005, 02:23:48 ; Search time 128.743 Seconds
(without alignments)
663.913 Million cell updates/sec

Title: US-09-745-792A-12

Perfect score: 1200
Sequence: 1 VPCVSGGLPKPANITFLSIN.....PSEKQCAITLKQSSSEFPKAK 221

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20038:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1200	100.0	221	4 AAB85269	AAB85269 Human IL-
2	1200	100.0	221	5 ABG67200	ABG67200 Human Int
3	1200	100.0	221	5 AAE23354	AAE23354 Human IL-
4	1200	100.0	221	8 ADJ83292	ADJ83292 Human IL-
5	1200	100.0	222	6 ABR42390	ABR42390 Human GCL
6	1200	100.0	542	4 AAU12265	AAU12265 Human PRO
7	1200	100.0	542	4 AAU29222	AAU29222 Human PRO
8	1200	100.0	542	6 ABU58598	ABU58598 Human PRO
9	1200	100.0	542	6 ABU88146	ABU88146 Novel hum
10	1200	100.0	542	6 ABR6335	ABR6335 Human sec
11	1200	100.0	542	6 ABR6335	ABR6335 Human sec
12	1200	100.0	542	6 ABR6335	ABR6335 Human sec
13	1200	100.0	542	6 ABR6335	ABR6335 Human sec
14	1200	100.0	542	6 ABR6335	ABR6335 Human sec
15	1200	100.0	542	6 ABR6335	ABR6335 Human sec
16	1200	100.0	542	6 ABR6335	ABR6335 Human sec
17	1200	100.0	542	6 ABR6335	ABR6335 Human sec
18	1200	100.0	542	6 ABR6335	ABR6335 Human sec
19	1200	100.0	542	6 ABR6335	ABR6335 Human sec
20	1200	100.0	542	6 ABR6335	ABR6335 Human sec
21	1200	100.0	542	6 ABR6335	ABR6335 Human sec
22	1200	100.0	542	6 ABR6335	ABR6335 Human sec
23	1200	100.0	542	6 ABR6335	ABR6335 Human sec
24	1200	100.0	542	6 ABR6335	ABR6335 Human sec
25	1200	100.0	542	6 ABR6335	ABR6335 Human sec

26	1200	100.0	542	6 ABU98151	ABU98151 Novel hum
27	1200	100.0	542	6 ABU80963	ABU80963 Human PRO
28	1200	100.0	542	6 ABU91857	ABU91857 Novel hum
29	1200	100.0	542	6 ABU89550	ABU89550 Human PRO
30	1200	100.0	542	6 ABU86391	ABU86391 Human sec
31	1200	100.0	542	6 ABU67604	ABU67604 Human sec
32	1200	100.0	542	6 ABU80632	ABU80632 Human PRO
33	1200	100.0	542	6 ABR9550	ABR9550 Human sec
34	1200	100.0	542	6 ABR9550	ABR9550 Human sec
35	1200	100.0	542	6 ABR9550	ABR9550 Human sec
36	1200	100.0	542	6 ABR9550	ABR9550 Human sec
37	1200	100.0	542	6 ABR9550	ABR9550 Human sec
38	1200	100.0	542	6 ABR9550	ABR9550 Human sec
39	1200	100.0	542	6 ABR9550	ABR9550 Human sec
40	1200	100.0	542	6 ABR9550	ABR9550 Human sec
41	1200	100.0	542	6 ABR9550	ABR9550 Human sec
42	1200	100.0	542	6 ABR9550	ABR9550 Human sec
43	1200	100.0	542	6 ABR9550	ABR9550 Human sec
44	1200	100.0	542	6 ABR9550	ABR9550 Human sec
45	1200	100.0	542	6 ABR9550	ABR9550 Human sec

ALIGNMENTS

RESULT 1
AAB85269
ID AAB85269 standard; protein; 221 AA.
XX
AC AAB85269;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human IL-20 receptor subunit IL-20RA extracellular domain fragment.
XX
KW Interleukin 20; IL-20; IL-20RA; Zeytor7; IL-20RB; DIRS1; immunoglobulin;
XX antiinflammatory; antiproliferative; antitumor; antitumor; antitumor;
XX dermatological; antitumor; antitumor; antitumor; antitumor; antitumor;
XX OS Homo sapiens.
XX
XX PN WO200146232-A2.
XX
XX PD 28-JUN-2001.
XX
XX PF 22-DEC-2000; 2000WO-US035307.
XX
XX PR 23-DEC-1999; 99US-00471774.
XX
XX PR 22-JUN-2000; 2000US-0213416P.
XX
XX PA (ZYMO) ZYMOGENETICS INC.
XX
XX PI Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
XX Rixon KW, Presnell SR, Fox BA;
XX WPI; 2001-398320/42.
XX
XX PT Isolated interleukin 20 soluble receptor comprising two polypeptide
XX subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
XX treating inflammatory diseases such as psoriasis.
XX
XX PS Claim 1; Page 65; 119pp; English.
XX
XX CC The invention relates to an interleukin 20 (IL-20) soluble receptor
XX comprising two polypeptide subunits IL-20RA (formerly known as Zeytor7)
XX and IL-20RB (formerly known as DIRS1). The two subunits are preferably
XX linked together. In one embodiment, one subunit is fused to the constant
XX region of the light chain of an immunoglobulin, and the other subunit is
XX fused to constant region of the heavy chain of an immunoglobulin. The
XX light chain and the heavy chain are connected via a disulfide bond. The
XX soluble receptor can be used to down-regulate IL-20 and thus treat
XX inflammatory diseases such as psoriasis, inflammatory lung injury such as
XX asthma or bronchitis, adult respiratory disease (ARD), septic shock,

CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact dermatitis, and inflammatory bowel disease such as ulcerative colitis and Crohn's disease. The present sequence represents a human IL-20 receptor and subunit IL-20RA extracellular domain fragment

CC Sequence 221 AA;

Query Match 100.0%; Score 1200; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.3e-112;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPCVSGGLPKPRANITFLSIMKNVLTQTPPEGLOGVYVTVYQYFYIGQKMLNKSCECN 60
DB 1 VPCVSGGLPKPRANITFLSIMKNVLTQTPPEGLOGVYVTVYQYFYIGQKMLNKSCECN 60
QY 61 INRTYCDLSAETSDYEHQYAKVKAIWGTRCSKMAESGRFPFLETOIGPEVALTTDEX 120
DB 61 INRTYCDLSAETSDYEHQYAKVKAIWGTRCSKMAESGRFPFLETOIGPEVALTTDEX 120
QY 121 SISVVLTAPEKMKRNPEDLVPSMQOITYSNLKNVSVLTNKSRTWSQCVTNHTLVLTWLE 180
DB 121 SISVVLTAPEKMKRNPEDLVPSMQOITYSNLKNVSVLTNKSRTWSQCVTNHTLVLTWLE 180
QY 181 PNTLYCVHVESFVGPERRAOPSEKOCARTLKDOGSEFFAK 221
DB 181 PNTLYCVHVESFVGPERRAOPSEKOCARTLKDOGSEFFAK 221

RESULT 2
ABG67200 standard; protein; 221 AA.

XX ABG67200;
XX 24-SEP-2002 (first entry)
DE Human Interleukin-20 sub-unit IL20RA mature extracellular domain.
XX

KM Inflammation; interleukin-20; IL-20; interleukin-8; IL-8; chemokine;
KM neutrophil; monocyte; basophil; eosinophil; chemotactic; psoriasis;
KM periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis;
KM angiogenesis-dependent chronic inflammatory condition; lung cancer;
KM melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract;
KM reperfusion injury; cancer; meningitis; rheumatic disease; skin disease;
KM idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis;
KM ulcerative colitis; eczema; atopic dermatitis; contact dermatitis;
KM inflammatory lung disease; AKD; adult respiratory disease; asthma;
KM bronchitis; pneumonia.

OS Homo sapiens.
XX
XX US2002042366-A1.
XX
XX 11-APR-2002.
XX
XX 22-DEC-2000; 2000US-00746359.
XX
XX 23-DEC-1999; 99US-0171969P.
XX
XX 22-JUN-2000; 2000US-0213341P.

PA (THOM/) THOMPSON P.
PA (POST/) FOSTER D C.
PA (XUW/) XU W.
PA (MADD/) MADDEN K L.
PA (KELLY/) KELLY J D.
PA (SPRE/) SPRECHER C A.
PA (BLUM/) BLUMBERG H.
PA (EAGA/) EAGAN M A.
PA (JASP/) JASPERS S R.
PA (CHAN/) CHANDRASEKHAR Y A.
PA (NOVA/) NOVAK J E.
PI Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;

PI Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;
XX WPI, 2002-507215/54.
XX

PT Treating inflammatory skin and lung diseases using antibodies against
PT Interleukins (IL)-20 (which indirectly modulates activation of IL-8),
PT useful for treating e.g. psoriasis, asthma and bronchitis.
XX

PS Disclosure, Page 21-22; 68pp; English.

XX The invention describes a method (I) for treating a mammal afflicted with
CC a disease in which an interleukin-20 (IL-20) polypeptide plays a role
CC comprising administering antagonist of the IL-20 polypeptide to the
CC individual. An important cytokine in the inflammatory process is
CC interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils
CC via chemotaxis and the release of granule enzymes. IL-8 binds to
CC receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is
CC a potent chemottractant for neutrophils, and the early stages of
CC periodontal disease are characterized by the influx of neutrophils. IL-8
CC is a potent inducer of angiogenesis in several angiogenesis-dependent
CC chronic inflammatory conditions, including rheumatoid arthritis,
CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an
CC important source of angiogenic activity in human lung cancer. Also, IL-8
CC expression correlates with experimental metastatic activity of some
CC melanoma cell lines. Therefore an effective method to treat inflammatory
CC diseases would be to administer an agent that would inhibit IL-8. It has
CC been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20
CC can be used to treat these diseases. The method is used for treating
CC diseases in which the IL-20 polypeptide plays a role e.g. inflammatory
CC diseases including diabetes, arteriosclerosis, cataracts, reperfusion
CC injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary
CC fibrosis, inflammatory bowel disease (ulcerative colitis), skin disease
CC (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an
CC inflammatory lung disease (adult respiratory disease (ARD), asthma,
CC bronchitis and pneumonia). This sequence represents a human interleukin-
XX 20 (IL-20) polypeptide used in developing the method of the invention

Sequence 221 AA;

Query Match 100.0%; Score 1200; DB 5; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.3e-112;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPCVSGGLPKPRANITFLSIMKNVLTQTPPEGLOGVYVTVYQYFYIGQKMLNKSCECN 60
DB 1 VPCVSGGLPKPRANITFLSIMKNVLTQTPPEGLOGVYVTVYQYFYIGQKMLNKSCECN 60
QY 61 INRTYCDLSAETSDYEHQYAKVKAIWGTRCSKMAESGRFPFLETOIGPEVALTTDEX 120
DB 61 INRTYCDLSAETSDYEHQYAKVKAIWGTRCSKMAESGRFPFLETOIGPEVALTTDEX 120
QY 121 SISVVLTAPEKMKRNPEDLVPSMQOITYSNLKNVSVLTNKSRTWSQCVTNHTLVLTWLE 180
DB 121 SISVVLTAPEKMKRNPEDLVPSMQOITYSNLKNVSVLTNKSRTWSQCVTNHTLVLTWLE 180
QY 181 PNTLYCVHVESFVGPERRAOPSEKOCARTLKDOGSEFFAK 221
DB 181 PNTLYCVHVESFVGPERRAOPSEKOCARTLKDOGSEFFAK 221

RESULT 3
AAE23354 standard; protein; 221 AA.

XX AAE23354;

XX 27-AUG-2002 (first entry)

XX Human IL-20RA mature extracellular protein.

XX Human; interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA;
KM Interleukin-20 receptor beta; IL-20RB; inflammation; arteriosclerosis;
KM diabetes; reperfusion injury; cancer; infectious meningitis; cataract;

KW rheumatoid arthritis; rheumatic fever; systemic lupus erythematosus;
KW antibacterial; cytostatic; dermatological; ophthalmological; vasotropic.
XX Homo sapiens.
XX WO200222153-A2.
XX
XX 21-MAR-2002.
XX
XX 13-SEP-2001; 2001WO-US028557.
XX
XX 15-SEP-2000; 2000US-0233305P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Chandrasekher YA, Jaepers SR;
XX
XX MPI; 2002-425815/45.
XX
XX Method of down-regulating IL-19 useful for treating inflammation
PT comprises administration of a polypeptide comprised of the extracellular
PT domain of IL-20RA and IL-20RB.
XX
XX Claim 2; Page 47-48; 80pp; English.
XX
XX The present invention relates to a method of down-regulating interleukin
CC (IL)-19. The method involves administration of a polypeptide comprised of
CC the extracellular domain of interleukin-20 receptor alpha (IL-20RA) and
CC the extracellular domain of interleukin-20 receptor beta (IL-20RB). The
CC IL-20RA and IL-20RB are heterodimeric receptors that bind to both IL-19
CC and mda7. The method is useful for down-regulating IL-19, useful for the
CC treatment of inflammation e.g., in diabetes, atherosclerosis, cataracts,
CC reperfusion injury, cancer, infectious meningitis, rheumatoid arthritis,
CC rheumatic fever and systemic lupus erythematosus. The present sequence is
CC human IL-20RA mature extracellular protein
XX
XX Sequence 221 AA;
SQ
Query Match 100.0%; Score 1200; DB 5; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.3e-112;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPCVSGGGLPKPANITFLSINMKNVLTQTPPEGLQGVKVTYTYQYFYGGKMLNSECN 60
DB 1 VPCVSGGGLPKPANITFLSINMKNVLTQTPPEGLQGVKVTYTYQYFYGGKMLNSECN 60
QY 61 INRTYCDLSAETSDYEHQYAKVKAIVGTCSKMAESGRFPFLETOIGPPEVALTTDEK 120
DB 61 INRTYCDLSAETSDYEHQYAKVKAIVGTCSKMAESGRFPFLETOIGPPEVALTTDEK 120
QY 121 SISVVLTAPEKWRNPEDLPVSMQOIYSNLKYNVSVLNTKSNRTWSQCVTHLTVLTWLE 180
DB 121 SISVVLTAPEKWRNPEDLPVSMQOIYSNLKYNVSVLNTKSNRTWSQCVTHLTVLTWLE 180
QY 181 PNTLYCVHVESFVPGPPRAQPSKQCAITLKDQSEFRAX 221
DB 181 PNTLYCVHVESFVPGPPRAQPSKQCAITLKDQSEFRAX 221
RESULT 4
ADJ83292
ID ADJ83292 standard; protein; 221 AA.
AC ADJ83292;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human IL-20RA subunit extracellular domain protein - SEQ ID 12.
XX
XX inflammation; single chain antibody; interleukin; IL-20; IL-20RA subunit;
KW IL-20RA subunit; antiinflammatory; dermatological; antipsoriatic;
KW antiaerthritic; respiratory; antiasthmatic; antidiabetic; antibacterial;
KW immunosuppressive; gastrointestinal; skin; psoriasis; eczema;

KW atopic dermatitis; contact dermatitis; lung;
KW adult respiratory distress syndrome; asthma; bronchitis; pneumonia;
KW arthritis; septic shock; multiple organ failure; bowel;
KW ulcerative colitis; Crohn's disease; human; receptor;
KW extracellular domain.
XX
XX Homo sapiens.
XX
XX US2004005320-A1.
XX
XX 08-JAN-2004.
XX
XX 28-APR-2003; 2003US-00424658.
XX
XX 23-DEC-1999; 99US-0171969P.
XX 22-JUN-2000; 2000US-0213341P.
XX 22-DEC-2000; 2000US-00746359.
XX
XX (THOM/) THOMPSON P.
XX (FOST/) FOSTER D C.
XX (XUW/) XU W.
XX (MADD/) MADDEN K L.
XX (KELL/) KELLY J D.
XX (SPRE/) SPRECHER C A.
XX (BLUM/) BLUMBERG H.
XX (EAG/) EAGAN M A.
XX (JASP/) JASPERS S R.
XX (CHAN/) CHANDRASEKHAR Y A.
XX (NOVA/) NOVAK J E.
XX
XX Thompson P, Foster DC, Xu W, Madden KU, Kelly JD, Sprecher CA,
PI Blumberg H, Eagan MA, Jaepers SR, Chandrasekher YA, Novak JE;
XX
XX MPI; 2004-081696/08.
XX
XX Reducing or treating inflammation, e.g. inflammatory lung disease,
PT comprises administering an antibody, antibody fragment or single chain
PT antibody that specifically binds to an interleukin (IL)-20RA subunit of
PT an IL-20 receptor.
XX
XX Disclosure; SEQ ID NO 12; 69pp; English.
XX
XX The invention relates to a novel method of reducing or treating
CC inflammation in a mammal which comprises administering an antibody,
CC antibody fragment or single chain antibody which specifically binds to a
CC receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-
CC 20RB subunit. The method of the invention has antiinflammatory,
CC dermatological, antipsoriatic, antiarthritic, respiratory, antiasthmatic,
CC antidiabetic, antibacterial, immunosuppressive and gastrointestinal
CC applications and may be useful for reducing or treating an inflammation,
CC including an inflammatory skin disease such as psoriasis, eczema, atopic
CC dermatitis and contact dermatitis or an inflammatory lung disease such as
CC adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as
CC well as arthritis, septic shock, multiple organ failure, inflammation
CC bowel disease, ulcerative colitis or Crohn's disease. The current
CC sequence is that of the human IL-20RA subunit-related protein of the
CC invention.
XX
XX Sequence 221 AA;
SQ
Query Match 100.0%; Score 1200; DB 8; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.3e-112;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPCVSGGGLPKPANITFLSINMKNVLTQTPPEGLQGVKVTYTYQYFYGGKMLNSECN 60
DB 1 VPCVSGGGLPKPANITFLSINMKNVLTQTPPEGLQGVKVTYTYQYFYGGKMLNSECN 60
QY 61 INRTYCDLSAETSDYEHQYAKVKAIVGTCSKMAESGRFPFLETOIGPPEVALTTDEK 120
DB 61 INRTYCDLSAETSDYEHQYAKVKAIVGTCSKMAESGRFPFLETOIGPPEVALTTDEK 120
QY 121 SISVVLTAPEKWRNPEDLPVSMQOIYSNLKYNVSVLNTKSNRTWSQCVTHLTVLTWLE 180

Db 121 SISVLTAPBEKKENPEDLPVSMQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 180
Oy 181 PNTLYCVHVESFVPPRRAPSPSEKOCARTLKDOSSSEFKAK 221
Db 181 PNTLYCVHVESFVPPRRAPSPSEKOCARTLKDOSSSEFKAK 221

RESULT 5
ABR42390
ID ABR42390 standard; protein; 222 AA.
XX
AC ABR42390;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human soluble interleukin-20 receptor subunit alpha.

XX
KW Human; interleukin-20; receptor; cytokine; signal transduction;
KW antiinflammatory; immunosuppressive; anti-HIV; antiallergic;
KW antiarteriosclerotic; neuroprotective; cardiovascular; cardiant;
KW thrombolytic; nephrotropic; haemostatic; cytostatic.
XX
OS Homo sapiens.

XX
PN WO2003035096-A1.
XX
PD 01-MAY-2003.
XX
PF 09-OCT-2002; 2002WO-US029844.
XX
PR 22-OCT-2001; 2001US-0342233P.
XX
PA (ELIL) LILLY & CO ELI.

XX
PI Baldwin DB, Rowlinson SW,
XX
DR WPI; 2003-421366/39.
XX
N-PSDB; ACCS8076.

XX
PT Treating or preventing inflammation, immune system, cardiovascular and
PT hematopoietic disorders, and regulation of cellular proliferation
PT comprises administering proteins inhibiting cytokine signalling, e.g.
PT LP338s or LP39s.

XX
PS Claim 1; Fig 1; 65pp; English.

XX
CC The present sequence is the protein sequence of the human soluble
CC interleukin-20 (IL20) receptor alpha subunit. The invention provides a
CC method for the treatment and/or prevention of inflammation, immune
CC system, cardiovascular and haematopoietic disorders and regulation of
CC cellular proliferation by inhibiting the binding of a cytokine (e.g.
CC interleukin-15, interleukin-20 and/or interleukin-24) to its receptor
CC complex, thereby preventing signal transduction. The method uses purified
CC soluble receptor proteins, such as the soluble IL20 receptor alpha
CC subunit. A pharmaceutical composition comprising the polypeptide, or a
CC fusion protein including the polypeptide, is useful for modulating the
CC physiology or development of a cell in vivo, in vitro and/or in situ
XX
SQ Sequence 222 AA;

Query Match 100.0%; Score 1200; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.3e-112;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VPCVSGGIPKPNATITFLSINKKNTVLTWTPPEGLQGVKVTYVQYFIYQKKMLNKKSCRN 60
Db 1 VPCVSGGIPKPNATITFLSINKKNTVLTWTPPEGLQGVKVTYVQYFIYQKKMLNKKSCRN 60
Oy 61 INRTYCDLSAETSDYEHQYAKVAKINWTKSKYAESGRFPFETQIGPEVALTTDEK 120
Db 61 INRTYCDLSAETSDYEHQYAKVAKINWTKSKYAESGRFPFETQIGPEVALTTDEK 120

Oy 121 SISVLTAPBEKKENPEDLPVSMQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 180
Db 121 SISVLTAPBEKKENPEDLPVSMQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 180
Oy 181 PNTLYCVHVESFVPPRRAPSPSEKOCARTLKDOSSSEFKAK 221
Db 181 PNTLYCVHVESFVPPRRAPSPSEKOCARTLKDOSSSEFKAK 221

RESULT 6
AAU12265
ID AAU12265 standard; protein; 542 AA.
XX
AC AAU12265;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO4978 polypeptide sequence.

XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.

XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.

XX
PR 01-DEC-1999; 99WO-US028301.
XX
PR 01-DEC-1999; 99WO-US028634.
XX
PR 02-DEC-1999; 99WO-US028551.
XX
PR 02-DEC-1999; 99WO-US028564.
XX
PR 09-DEC-1999; 99WO-US028565.
XX
PR 16-DEC-1999; 99US-0170262P.
XX
PR 20-DEC-1999; 99WO-US030095.
XX
PR 20-DEC-1999; 99WO-US030911.
XX
PR 30-DEC-1999; 99WO-US030999.
XX
PR 30-DEC-1999; 99WO-US031243.
XX
PR 05-JAN-2000; 99WO-US031274.
XX
PR 06-JAN-2000; 2000WO-US000219.
XX
PR 06-JAN-2000; 2000WO-US000277.
XX
PR 11-FEB-2000; 2000WO-US003565.
XX
PR 18-FEB-2000; 2000WO-US004341.
XX
PR 18-FEB-2000; 2000WO-US004342.
XX
PR 22-FEB-2000; 2000WO-US004414.
XX
PR 24-FEB-2000; 2000WO-US004914.
XX
PR 24-FEB-2000; 2000WO-US005004.
XX
PR 01-MAR-2000; 2000WO-US005601.
XX
PR 02-MAR-2000; 2000WO-US005841.
XX
PR 03-MAR-2000; 2000US-0187202P.
XX
PR 10-MAR-2000; 2000WO-US006319.
XX
PR 15-MAR-2000; 2000WO-US006884.
XX
PR 20-MAR-2000; 2000WO-US007377.
XX
PR 21-MAR-2000; 2000WO-US007532.
XX
PR 30-MAR-2000; 2000WO-US008439.
XX
PR 17-MAY-2000; 2000WO-US013705.
XX
PR 22-MAY-2000; 2000WO-US014042.
XX
PR 30-MAY-2000; 2000WO-US014941.
XX
PR 02-JUN-2000; 2000WO-US015264.
XX
PR 05-JUN-2000; 2000US-0209832P.
XX
PR 28-JUL-2000; 2000WO-US020710.
XX
PR 11-AUG-2000; 2000WO-US022031.
XX
PR 23-AUG-2000; 2000WO-US023522.
XX
PR 24-AUG-2000; 2000WO-US023328.
XX
PR 08-NOV-2000; 2000WO-US030952.
XX
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI, 2001-408281/43.
 N-PSDB; AAS21337.
 XX
 DR
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 12; Fig 188; 813pp; English.
 PS
 XX
 CC AAU2172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIa. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 542 AA;
 Query Match 100.0%; Score 1200; DB 4; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1,2e-111;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPCVSGGLPKRANITFLSINKNVLQWTPPEGLQGVKVTYVYFYGGKMLNKSECN 60
 DB 19 VPCVSGGLPKRANITFLSINKNVLQWTPPEGLQGVKVTYVYFYGGKMLNKSECN 78
 QY 61 INRTYCDLSAETSDYEHQYAKVKAIGTKCKNAESGFRFPLETOIGPPEVALTTDEK 120
 DB 79 INRTYCDLSAETSDYEHQYAKVKAIGTKCKNAESGFRFPLETOIGPPEVALTTDEK 138
 QY 121 SISVVLTAPEKWRAPEDLPVSMQOISNLTKNVSVLNTKSNRTWSQCVTNHTLVLTMLE 180
 DB 139 SISVVLTAPEKWRAPEDLPVSMQOISNLTKNVSVLNTKSNRTWSQCVTNHTLVLTMLE 198
 QY 181 PNTLYCVAVESFVPGPPRRAQPSKQCAATTLKQSSSEPRAX 221
 DB 199 PNTLYCVAVESFVPGPPRRAQPSKQCAATTLKQSSSEPRAX 239

RESULT 7
 AAU29222
 ID AAU29222 standard; protein; 542 AA.
 XX
 AC AAU29222;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #199.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX OS Homo sapiens.
 XX
 XX
 PN WO20016848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006520.
 XX
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
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 PR 28-MAR-2000; 2000US-0192655P.
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 PR 30-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
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 PR 11-APR-2000; 2000US-0196000P.
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 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-0064848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI, 2001-602746/68.
 DR N-PSDB; AAS46123.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 PS Claim 11; Fig 398; 774pp; English.
 PS
 XX
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate

CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 542 AA;

Query Match 100.0%; Score 1200; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 1,2e-111;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VPCVSGGLPKRANITTFISINKNTLVQTPPEGLQGVVYTYVYFYIGQKKMLNKSECRN 60
Db 19 VPCVSGGLPKRANITTFISINKNTLVQTPPEGLQGVVYTYVYFYIGQKKMLNKSECRN 78
QY 61 INRTYCDLSAETSYEHQYAKYKVAIMGTCKSKMAEGRRYPLETOIGPPEVALTTDEK 120
Db 79 INRTYCDLSAETSYEHQYAKYKVAIMGTCKSKMAEGRRYPLETOIGPPEVALTTDEK 138
QY 121 SISVVLTAPEKKRNPEDLPVSMQOIYSNLKYNVSVLNTSKNRTWSQCVTNHTLVLTWLE 180
Db 139 SISVVLTAPEKKRNPEDLPVSMQOIYSNLKYNVSVLNTSKNRTWSQCVTNHTLVLTWLE 198
QY 181 PNTLYCHVESFPVGPERRAQSEKOCARTLKQSSSEFPYAK 221
Db 199 PNTLYCHVESFPVGPERRAQSEKOCARTLKQSSSEFPYAK 239
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RESULT 8
ABUS8598
ID ABUS8598 standard; protein; 542 AA.
XX

AC ABUS8598;

XX 15-APR-2003 (first entry)

DE Human PRO polypeptide #199.

XX Human PRO; cytosol; cancer; breast; lung; stomach; liver;

KM dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;

KW antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

OS US2003027272-A1.

XX 06-FEB-2003.

PD 21-JUN-2002; 2002US-00176492.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

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PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

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PR 11-MAR-1998; 98US-0077632P.

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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1200; DB 6; Length 542;
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Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 199 PNTLYCVHESFVPGPPRRAPQSEKQARTLKDQSSSEFKAK 239
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RESULT 9
ABU88146
ID ABU88146 standard; protein, 542 AA.
XX AC ABU88146;
XX DT 07-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO4978.
XX DE Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW Chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN US2003032127-A1.
XX PD 13-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183012.
XX XX
PR 18-SEP-1997; 97US-0059263P.
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PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
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PR 18-AUG-1998; 98US-0096949P.
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PR 02-SEP-1998; 98US-0098803P.
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PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
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PR 18-SEP-1998; 98US-0100830P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
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PR 06-OCT-1998; 98US-0103258P.

Query Match 100.0%; Score 1200; DB 6; Length 542;
Best Local Similarity 100.0%; Pred. No. 1,2e-111;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPCVSGGLPKPKNITFLSINMKNVQTPPEGLQGVKTYTYQYFIYQKKKLNKSEGN 60
DB 19 VPCVSGGLPKPKNITFLSINMKNVQTPPEGLQGVKTYTYQYFIYQKKKLNKSEGN 78
QY 61 INRTYCDLSAETSDYEHQYAKVKAIWGTCKSKMAESGRFPELETQIGPPEVALTTDEK 120
DB 79 INRTYCDLSAETSDYEHQYAKVKAIWGTCKSKMAESGRFPELETQIGPPEVALTTDEK 138
QY 121 SISVVLTAPEKKNRPEDLPVSMQIYSNLKYNVSVLNTKSNRTWSOCVTNHTLVLTWLE 180
DB 139 SISVVLTAPEKKNRPEDLPVSMQIYSNLKYNVSVLNTKSNRTWSOCVTNHTLVLTWLE 198
QY 181 PNTLYCVAVESVFPGRRAQSEKQCARLTLDQSESEFQAK 221
DB 199 PNTLYCVAVESVFPGRRAQSEKQCARLTLDQSESEFQAK 239

RESULT 10

ID AB084461 standard; protein; 542 AA.

AC AB084461;

DT 02-AUG-2003 (first entry)

DE Human secreted/transmembrane protein (PRO) #199.

KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.

OS Homo sapiens.

PN US2003032112-A1.

PD 13-FEB-2003.

PF 21-JUN-2002; 2002US-00176756.

PR 18-SEP-1997; 97US-0059263P.

PR 17-OCT-1997; 97US-0059266P.

PR 21-OCT-1997; 97US-0063250P.

PR 24-OCT-1997; 97US-0063486P.

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PR 12-JUN-1998; 98US-0089105P.

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PR	23-SEP-1998;	98US-01014716
PR	23-SEP-1998;	98US-01014722
PR	23-SEP-1998;	98US-01014752
PR	23-SEP-1998;	98US-01014772
PR	24-SEP-1998;	98US-01017388
PR	24-SEP-1998;	98US-01017398
PR	24-SEP-1998;	98US-01017399
PR	24-SEP-1998;	98US-01017430
PR	25-SEP-1998;	98US-01019232
PR	25-SEP-1998;	98US-01017868
PR	26-SEP-1998;	98US-01022070
PR	29-SEP-1998;	98US-01022076
PR	29-SEP-1998;	98US-01023300
PR	29-SEP-1998;	98US-01023310
PR	30-SEP-1998;	98US-01024670
PR	30-SEP-1998;	98US-01025700
PR	30-SEP-1998;	98US-01025710
PR	01-OCT-1998;	98US-01026640
PR	01-OCT-1998;	98US-01026870
PR	02-OCT-1998;	98US-01029650
PR	06-OCT-1998;	98US-01032580
PR	06-OCT-1998;	98US-01034490
PR	07-OCT-1998;	98US-01068378

Query Match	100.0%;	Score 1200;	DB 6;	length 542;
Best Local Similarity	100.0%;	Pred. No. 1.2e-111;		
Matches 221; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	VPCVSGGLGKRPANITPFLSTIMKKNVLQMPPEGLQSVKTYTVQVFIYIGQKKMLKNSCRN	60
Db	19	VPCVSGGLGKRPANITPFLSTIMKKNVLQMPPEGLQSVKTYTVQVFIYIGQKKMLKNSCRN	78
QY	61	INRTYCDLSAETSDYEHQYAKYKAIWTKCSKNAESGRFPYLETQIGPPEVALITDEK	120
Db	79	INRTYDDLSAETSDYEHQYAKYKAIWTKCSKNAESGRFPYLETQIGPPEVALITDEK	138
QY	121	SISVVLTADEKMKRNPEDLPVSMQOISYLNLTKNYSVLNTKSNRTWCSQVTHLTVLTWLE	180
Db	139	SISVVLTADEKMKRNPEDLPVSMQOISYLNLTKNYSVLNTKSNRTWCSQVTHLTVLTWLE	198
QY	181	PNTLYCVHVESFVPGPPRPAQSEKQCARLTLDQSSSEPKAK	221
Db	199	PNTLYCVHVESFVPGPPRPAQSEKQCARLTLDQSSSEPKAK	239

RESULT	11
ABR66335	
ID	ABR66335 standard; protein; 542 AA.
XX	
AC	ABR66335;
XX	
DE	05-AUG-2003 (first entry)
DT	
XX	
XX	Human secreted polypeptide PRO4978, SEQ ID NO:398.
KW	Human; PRO; secreted protein; transmembrane protein;
KW	extracellular domain; tumour necrosis factor-alpha;
KW	chondrocyte; proliferation; differentiation; cartilage disorder;
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW	liver; drug screening; transgenic animal; genetic analysis;
KW	antiarthritic; vulnery; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	US2003027278-A1.
XX	
PD	06-FEB-2003.
XX	
PF	21-JUN-2002; 2002US-00176987.
XX	
PR	18-SEP-1997; 97US-0059263P.
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NR	18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
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PR 10-AUG-1998; 98US-0095998P.
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PR 17-AUG-1998; 98US-0096757P.
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PR 18-AUG-1998; 98US-0096959P.
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PR 01-OCT-1998; 98US-0102684P.
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Query Match 100.0%; Score 1200; DB 6; Length 542;
Best Local Similarity 100.0%; Pred. No. 1,2e-111;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPCVSGGLPKPANITFLSINMKNVLTQTPPEGLQGVKVVYVYQFYIGQKMLNKSECN 60
DB 19 VPCVSGGLPKPANITFLSINMKNVLTQTPPEGLQGVKVVYVYQFYIGQKMLNKSECN 78
QY 61 INRTYCDLSAETSDYHOYAYAKAIWGTCKSKMAESGFPYPLETOIQEPPEVALTTDEK 120
DB 79 INRTYCDLSAETSDYHOYAYAKAIWGTCKSKMAESGFPYPLETOIQEPPEVALTTDEK 138
QY 121 SISVVLTAPEKMKRNEDLPVSMQOITYSNLKTNVSVLNTKSNRTMSQCVTHTLVLTWLE 180
DB 139 SISVVLTAPEKMKRNEDLPVSMQOITYSNLKTNVSVLNTKSNRTMSQCVTHTLVLTWLE 198
QY 181 PNTLYCVHVESFVPGPPRAQPSKQCAFTLKDQSEFPYAK 221
DB 199 PNTLYCVHVESFVPGPPRAQPSKQCAFTLKDQSEFPYAK 239

RESULT 12
ABR65725

ID ABR65725 standard; protein; 542 AA.

AC ABR65725;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO4978, SEQ ID NO:398.

KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antithrilitic; vulnerary; gene therapy.

OS Homo sapiens.

XX US2003036159-A1.

XX 20-FEB-2003.

PD

XX 02-JUL-2002; 2002US-00188773.
PF 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
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PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
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PR 24-NOV-1997; 97US-0066466P.
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XX 27-JUN-2002; 2002US-00184627.
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Query Match 100.0%; Score 1200; DB 6; Length 542;
 Best Local Similarity 100.0%; Pred. No. 1.2e-111;

Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 INRTYCDLSAETSDYEHQYAVKAIWGTCKSKMAESGRFYPLETQICPPEVALTTDEK 120
 DB 79 INRTYCDLSAETSDYEHQYAVKAIWGTCKSKMAESGRFYPLETQICPPEVALTTDEK 138
 QY 121 SISVVLTAPEKKRRPDEDLVSMQOIYSMLKKNVSLTNKSNRTWSQCVTNHTLVLTWLE 180
 DB 139 SISVVLTAPEKKRRPDEDLVSMQOIYSMLKKNVSLTNKSNRTWSQCVTNHTLVLTWLE 198
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 DB 199 PNTLYCVHVESFVPGPRRAQSEKQCATLTKDQSEFFAK 239

RESULT 14

ID ABU82904
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AC ABU82904;

XX 27-JUN-2003 (first entry)

DE Human PRO polypeptide #199.

KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;

KX Chromosome mapping; gene mapping; cytostatic.

OS Homo sapiens.
 XX US2003032113-A1.
 PN 13-FEB-2003.
 PD 20-JUN-2002; 2002US-00176911.
 XX 18-SEP-1997; 97US-0059263P.
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Best Local Similarity 100.0%; Pred. No. 1,2e-111; Indels 0; Gaps 0;
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QY 61 INRTYCDLSAETSDEHYAVKAIWGTCKSKMAESGRFYFLETOIGPPEVALTTDEK 120
DB 79 INRTYCDLSAETSDEHYAVKAIWGTCKSKMAESGRFYFLETOIGPPEVALTTDEK 138
QY 121 SISVITLAPKWKRPEDIPVSMQIYSNLKXTNVSVLTKNSRKTWSQCVTNHTLVLTWE 180
DB 139 SISVITLAPKWKRPEDIPVSMQIYSNLKXTNVSVLTKNSRKTWSQCVTNHTLVLTWE 198
QY 181 PNTLYCVHVESFVPPRRRAQSEKQCARTLKDQSEKFAK 221
DB 199 PNTLYCVHVESFVPPRRRAQSEKQCARTLKDQSEKFAK 239

RESULT 15
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ID AB017709 strand, protein, 542 AA.
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AC AB017709;
XX
DT 26-AUG-2003 (first entry)
XX

DE Novel human secreted and transmembrane protein PRO4978.
 XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiatic; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
 KW bioreactor; tissue typing.
 XX Homo sapiens.
 OS
 PN US2003032156-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 06-MAY-2002; 2002US-00140474.
 XX
 PR 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUN-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019433.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022992.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005150.
 PR 20-APR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 30-NOV-1999; 98WO-US028409.
 PR 01-DEC-1999; 98WO-US028301.
 PR 01-DEC-1999; 98WO-US028634.
 PR 02-DEC-1999; 98WO-US028551.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030035.
 PR 20-DEC-1999; 98WO-US030911.
 PR 22-DEC-1999; 98WO-US030959.
 PR 30-DEC-1999; 98WO-US030720.
 PR 30-DEC-1999; 98WO-US031243.
 PR 05-JAN-2000; 98WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.

PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 16-AUG-2001; 2001US-00927796.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 XX (GENTH) GENENTECH INC.
 PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
 XX
 XX WPI; 2003-341980/32.
 DR N-Psdb; ACD23946.
 XX
 PT New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.
 XX
 PS Claim 12; Fig 188; 660pp; English.
 XX
 CC The invention describes an isolated nucleic acid (I) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (I) is used to
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit

CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX

Sequence 542 AA;

Query Match 100.0%; Score 1200; DB 6; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.2e-111;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPCVSGGLPKPANTTFISIMKNVLQWTPPEGLQGVKVTYTVQYFIYGOKWLNKSECRN 60
DB 19 VPCVSGGLPKPANTTFISIMKNVLQWTPPEGLQGVKVTYTVQYFIYGOKWLNKSECRN 78
QY 61 INRTYCDLSAETSDYEHQYAKYKATWGTCSCMAESGRFPLETOIGPPEVALTTDEK 120
DB 79 INRTYCDLSAETSDYEHQYAKYKATWGTCSCMAESGRFPLETOIGPPEVALTTDEK 138
QY 121 SISVVLTAPEKMKRNPEDLFVSMQOISNLYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 180
DB 139 SISVVLTAPEKMKRNPEDLFVSMQOISNLYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 198
QY 181 PNTLYCVHWESFVPGPPRRAQPESEKOCARTLKDQSSSEFPAK 221
DB 199 PNTLYCVHWESFVPGPPRRAQPESEKOCARTLKDQSSSEFPAK 239

Search completed: February 25, 2005, 02:39:44
Job time : 132.743 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2005, 02:33:14 ; Search time 25.5401 Seconds
(without alignments)
832.570 Million cell updates/sec

Title: US-09-745-792a-12

Perfect score: 1200
Sequence: 1 VPCVSGGLKRPANITFLSLN.....PSEKQARTLKQSSSEPKAK 221

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	232.5	19.4	325	2 A47003	cytokine receptor
2	230.5	19.2	349	2 JG6311	interferon recepto
3	196	16.3	590	2 A45283	interferon alpha/b
4	186.5	15.5	560	2 S27387	interferon alpha x
5	168.5	14.0	557	2 A32694	interferon gamma/b
6	163.5	13.6	489	2 A31555	interferon gamma r
7	159	13.2	575	2 A49667	interleukin-10 rec
8	143	11.9	578	2 I56215	interleukin-10 rec
9	138.5	11.5	332	2 A49947	interferon gamma r
10	137	11.4	477	2 A34368	interferon gamma r
11	136.5	11.3	337	2 I38500	interferon gamma r
12	135.5	11.4	295	1 KFRH3	tissue factor prec
13	131.5	11.0	294	1 KFM53	tissue factor prec
14	130	10.8	292	1 KFRB3	tissue factor prec
15	129	10.8	282	1 KFRB3	tissue factor prec
16	118.5	9.9	26926	1 I38344	titin, cardiac mus
17	115	9.6	515	2 I39073	interferon alpha-b
18	112	9.3	331	2 A54295	interferon alpha/b
19	112	9.3	331	2 S59501	interferon recepto
20	109.5	9.1	896	2 I56562	interleukin-3 rece
21	105.5	8.8	896	1 A35782	cytokine receptor
22	101	8.4	917	2 I49699	glycoprotein 130 -
23	100.5	8.4	2302	2 T14328	protein-tyrosine-p
24	98.5	8.2	976	2 A36355	hypothetical prote
25	95.5	8.0	1014	2 T24412	hypothetical prote
26	95.5	8.0	1091	2 S01998	contactin precurs
27	95.5	8.0	2215	2 T00348	LR11 protein - mou
28	94.5	7.9	266	2 T28607	hypothetical prote
29	94.5	7.9	266	2 H72172	H9R protein - vari

30	93.5	7.8	266	2 I36855	gene B9R protein -
31	93.5	7.8	6658	2 T13931	prolactin - fruit
32	91.5	7.6	272	2 JQ1802	BBR 31K protein pr
33	91.5	7.6	2029	1 TDFPLK	protein-tyrosine-p
34	90	7.5	1344	2 T14316	rig-1 protein - mo
35	90	7.5	1375	2 T13822	frizzled gene prot
36	90	7.5	1526	2 T19473	hypothetical prote
37	90	7.5	1526	2 T13823	frizzled gene prot
38	89.5	7.5	1897	1 TDH1LK	leukocyte antigen-
39	89.5	7.5	1898	2 S46216	leukocyte antigen-
40	89	7.4	897	1 A39255	cytokine receptor
41	88.5	7.4	272	2 G42526	BBR protein - vacc
42	88.5	7.4	977	2 S49004	tyrosine kinase Mp
43	88	7.3	948	2 S51605	receptor-like tyro
44	86.5	7.2	440	2 I50213	protein-tyrosine-p
45	86.5	7.2	525	2 E86463	hypothetical prote

ALIGNMENTS

RESULT 1

A47003
Cytokine receptor family class II protein CRP2-4 precursor - human
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: A47003; G01418
R/Lutfalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A/Title: A new member of the cytokine receptor gene family maps on chromosome 21 at 16p.
A/Reference number: A47003; PMID:93300510; PMID:8314576
A/Accession: A47003
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-325 <LUT>
A/Cross-references: UNIPROT:Q08334; GB:Z17227; NID:G393378; PIDN:CAA78933.1; PID:G393377
R/Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A/Reference number: G06935
A/Accession: G01418
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-123, 'D', 125-268, 'VGMR' <LUT>
A/Cross-references: EMBL:U08988; NID:G571295; PID:G571296
C/Genetics:
A/Gene: GDB:CRP4; CRP2-4
A/Cross-references: GDB:138168; OMIM:123889
A/Map position: 21q, 21q22.1-21q22.2
A/Intons: 17/1; 58/2; 111/1; 166/3; 216/1
C/Keywords: transmembrane protein

Query Match 19.4%; Score 232.5; DB 2; Length 325;
Best Local Similarity 29.2%; Pred. No. 3.9e-12;
Matches 63; Conservative 36; Mismatches 94; Indels 23; Gaps 6;

Qy	6	GGLPKPNITFLSLNKKNVLTQTPPBGLOQVTVYQVYIGQKMLNKGNNIRTY	65
Db	19	GMVPPENVMNVNKNILQWESPAFKG-NITFLAQVLSYR-----IPDCKNTTLTE	73
Qy	66	CDLSAETSDYEHQYAKVAKIWTGCKSKMAESGRFPPELTQIGPPEVALTTBEKISV	125
Db	74	CDSSLSKYGDHT--LRVRAEFADHSDWNI--TFCPVDDTIIGPDMQVEVLADSIAMR	130
Qy	126	LTAP-----EKKNRPEDLPVSMQQLYSVLKXNVSLNKSRTWSQCTNHTLVITWL	179
Db	131	FLAPKLENEYETV-----TKQVYNSWTNVQVKNQGTDEKFIQTPQYDFEVLRL	181
Qy	180	EPNTLYCVHVESFVPGPPRAQPSKQACARTLKDS	215
Db	182	EPWTTCVQVRGFLPDRNKAQSEVCEGTTHDET	217

RESULT 2

JC6311
 Interferon receptor class II cytokine receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: J06311
 R/Gibbs, V.C.; Pennica, D.
 Gene 186, 97-101, 1997
 A/Title: CRP2-4: isolation of cDNA clones encoding the human and mouse proteins.
 A/Reference number: J06311; MUID:97199375; PMID:9047351
 A/Accession: J06311
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-349 <GIB>
 A/Cross-references: UNIPROT:O8VHM7; GB:U53696

Query Match 19.2%; Score 230.5; DB 2; Length 349;
 Best Local Similarity 29.8%; Pred. No. 6,3e-12;
 Matches 67; Conservative 35; Mismatches 100; Indels 23; Gaps 8;
 QY 2 PCVSGGL-----PKRANITPLSINMKNVLTQWTPPEGLQGVKVTYTYQYFIYQ 49
 DB 3 PCVAGMLGGLFLVPALGMIPPEKVRMNSVNFKNILQWEVP-APPKNTLTFTAQYESYRS 61
 QY 50 KKWINKSECRNINFRYCDLSAFTSDYEHQYAKYKAIWGTCKSKMAESGRFPPELTQIG 109
 DB 62 ----FQDHCKRTASTQCDPS-HLSKY-GDYTVRVRAELADBSHSEWV-NVTEFCPEVDITIG 114
 QY 110 PPEVALTTDEKISIVLTPAPEKMKRNPEDLFVSMQOYSLNKYVSVLNTKSNRTWQCV 169
 DB 115 PPEMIGESLASLSEHRSAPQ-INEEPTM-TLKATYDSWAKYVQYWKNGTNEKFPQVS 171
 QY 170 TNNHVLVLTWLEPNTLYCVHVESFVGPERRAOPSEKOCARTLKDQ 214
 DB 172 PYDESVLRNLEPMTTYCIVQGVFLDQNRGTGEMSEPICERTGNDE 216

RESULT 3

A45283
 Interferon alpha/beta receptor - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
 R/Uze, G.; Luftalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
 A/Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homospere
 A/Reference number: A45283; MUID:92262522; PMID:1533935
 A/Accession: A45283
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-590 <UZE>
 A/Cross-references: UNIPROT:P33896; GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112
 R/Luftalla, G.; Uze, G.
 Gene 148, 343-346, 1994
 A/Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq
 A/Reference number: I48423; MUID:95047447; PMID:7558966
 A/Accession: I48423
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 118-125 <RES>
 A/Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
 A/Accession: I48424
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 127-224 <RE2>
 A/Cross-references: EMBL:U06238; NID:g497104; PIDN:AAAC01749.1; PID:g755811
 A/Accession: I48425
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 243-264 <RE3>
 A/Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
 A/Accession: I48426
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 265-375 <RE4>
 A/Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
 A/Accession: I48427
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 397-424 <RE5>
 A/Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
 A/Accession: I48428
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 426-445 <RE6>
 A/Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
 A/Accession: I48429
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 473-590 <RE7>
 A/Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
 A/Accession: I48430
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 591-610 <RE8>
 A/Cross-references: EMBL:U06245; NID:g497115; PIDN:AAA65009.1; PID:g510266
 A/Accession: I48431
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 611-630 <RE9>
 A/Cross-references: EMBL:U06246; NID:g497116; PIDN:AAA65010.1; PID:g510267
 A/Accession: I48432
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 631-650 <RE10>
 A/Cross-references: EMBL:U06247; NID:g497117; PIDN:AAA65011.1; PID:g510268
 A/Accession: I48433
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 651-670 <RE11>
 A/Cross-references: EMBL:U06248; NID:g497118; PIDN:AAA65012.1; PID:g510269
 A/Accession: I48434
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 671-690 <RE12>
 A/Cross-references: EMBL:U06249; NID:g497119; PIDN:AAA65013.1; PID:g510270
 A/Accession: I48435
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 691-710 <RE13>
 A/Cross-references: EMBL:U06250; NID:g497120; PIDN:AAA65014.1; PID:g510271
 A/Accession: I48436
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 711-730 <RE14>
 A/Cross-references: EMBL:U06251; NID:g497121; PIDN:AAA65015.1; PID:g510272
 A/Accession: I48437
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 731-750 <RE15>
 A/Cross-references: EMBL:U06252; NID:g497122; PIDN:AAA65016.1; PID:g510273
 A/Accession: I48438
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 751-770 <RE16>
 A/Cross-references: EMBL:U06253; NID:g497123; PIDN:AAA65017.1; PID:g510274
 A/Accession: I48439
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 771-790 <RE17>
 A/Cross-references: EMBL:U06254; NID:g497124; PIDN:AAA65018.1; PID:g510275
 A/Accession: I48440
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 791-810 <RE18>
 A/Cross-references: EMBL:U06255; NID:g497125; PIDN:AAA65019.1; PID:g510276
 A/Accession: I48441
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 811-830 <RE19>
 A/Cross-references: EMBL:U06256; NID:g497126; PIDN:AAA65020.1; PID:g510277
 A/Accession: I48442
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 831-850 <RE20>
 A/Cross-references: EMBL:U06257; NID:g497127; PIDN:AAA65021.1; PID:g510278
 A/Accession: I48443
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 851-870 <RE21>
 A/Cross-references: EMBL:U06258; NID:g497128; PIDN:AAA65022.1; PID:g510279
 A/Accession: I48444
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 871-890 <RE22>
 A/Cross-references: EMBL:U06259; NID:g497129; PIDN:AAA65023.1; PID:g510280
 A/Accession: I48445
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 891-910 <RE23>
 A/Cross-references: EMBL:U06260; NID:g497130; PIDN:AAA65024.1; PID:g510281
 A/Accession: I48446
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 911-930 <RE24>
 A/Cross-references: EMBL:U06261; NID:g497131; PIDN:AAA65025.1; PID:g510282
 A/Accession: I48447
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 931-950 <RE25>
 A/Cross-references: EMBL:U06262; NID:g497132; PIDN:AAA65026.1; PID:g510283
 A/Accession: I48448
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 951-970 <RE26>
 A/Cross-references: EMBL:U06263; NID:g497133; PIDN:AAA65027.1; PID:g510284
 A/Accession: I48449
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 971-990 <RE27>
 A/Cross-references: EMBL:U06264; NID:g497134; PIDN:AAA65028.1; PID:g510285
 A/Accession: I48450
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 991-1010 <RE28>
 A/Cross-references: EMBL:U06265; NID:g497135; PIDN:AAA65029.1; PID:g510286
 A/Accession: I48451
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1011-1030 <RE29>
 A/Cross-references: EMBL:U06266; NID:g497136; PIDN:AAA65030.1; PID:g510287
 A/Accession: I48452
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1031-1050 <RE30>
 A/Cross-references: EMBL:U06267; NID:g497137; PIDN:AAA65031.1; PID:g510288
 A/Accession: I48453
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1051-1070 <RE31>
 A/Cross-references: EMBL:U06268; NID:g497138; PIDN:AAA65032.1; PID:g510289
 A/Accession: I48454
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1071-1090 <RE32>
 A/Cross-references: EMBL:U06269; NID:g497139; PIDN:AAA65033.1; PID:g510290
 A/Accession: I48455
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1091-1110 <RE33>
 A/Cross-references: EMBL:U06270; NID:g497140; PIDN:AAA65034.1; PID:g510291
 A/Accession: I48456
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1111-1130 <RE34>
 A/Cross-references: EMBL:U06271; NID:g497141; PIDN:AAA65035.1; PID:g510292
 A/Accession: I48457
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1131-1150 <RE35>
 A/Cross-references: EMBL:U06272; NID:g497142; PIDN:AAA65036.1; PID:g510293
 A/Accession: I48458
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1151-1170 <RE36>
 A/Cross-references: EMBL:U06273; NID:g497143; PIDN:AAA65037.1; PID:g510294
 A/Accession: I48459
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1171-1190 <RE37>
 A/Cross-references: EMBL:U06274; NID:g497144; PIDN:AAA65038.1; PID:g510295
 A/Accession: I48460
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1191-1210 <RE38>
 A/Cross-references: EMBL:U06275; NID:g497145; PIDN:AAA65039.1; PID:g510296
 A/Accession: I48461
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1211-1230 <RE39>
 A/Cross-references: EMBL:U06276; NID:g497146; PIDN:AAA65040.1; PID:g510297
 A/Accession: I48462
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1231-1250 <RE40>
 A/Cross-references: EMBL:U06277; NID:g497147; PIDN:AAA65041.1; PID:g510298
 A/Accession: I48463
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1251-1270 <RE41>
 A/Cross-references: EMBL:U06278; NID:g497148; PIDN:AAA65042.1; PID:g510299
 A/Accession: I48464
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1271-1290 <RE42>
 A/Cross-references: EMBL:U06279; NID:g497149; PIDN:AAA65043.1; PID:g510300
 A/Accession: I48465
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1291-1310 <RE43>
 A/Cross-references: EMBL:U06280; NID:g497150; PIDN:AAA65044.1; PID:g510301
 A/Accession: I48466
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1311-1330 <RE44>
 A/Cross-references: EMBL:U06281; NID:g497151; PIDN:AAA65045.1; PID:g510302
 A/Accession: I48467
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1331-1350 <RE45>
 A/Cross-references: EMBL:U06282; NID:g497152; PIDN:AAA65046.1; PID:g510303
 A/Accession: I48468
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1351-1370 <RE46>
 A/Cross-references: EMBL:U06283; NID:g497153; PIDN:AAA65047.1; PID:g510304
 A/Accession: I48469
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1371-1390 <RE47>
 A/Cross-references: EMBL:U06284; NID:g497154; PIDN:AAA65048.1; PID:g510305
 A/Accession: I48470
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1391-1410 <RE48>
 A/Cross-references: EMBL:U06285; NID:g497155; PIDN:AAA65049.1; PID:g510306
 A/Accession: I48471
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1411-1430 <RE49>
 A/Cross-references: EMBL:U06286; NID:g497156; PIDN:AAA65050.1; PID:g510307
 A/Accession: I48472
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1431-1450 <RE50>
 A/Cross-references: EMBL:U06287; NID:g497157; PIDN:AAA65051.1; PID:g510308
 A/Accession: I48473
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1451-1470 <RE51>
 A/Cross-references: EMBL:U06288; NID:g497158; PIDN:AAA65052.1; PID:g510309
 A/Accession: I48474
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1471-1490 <RE52>
 A/Cross-references: EMBL:U06289; NID:g497159; PIDN:AAA65053.1; PID:g510310
 A/Accession: I48475
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1491-1510 <RE53>
 A/Cross-references: EMBL:U06290; NID:g497160; PIDN:AAA65054.1; PID:g510311
 A/Accession: I48476
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1511-1530 <RE54>
 A/Cross-references: EMBL:U06291; NID:g497161; PIDN:AAA65055.1; PID:g510312
 A/Accession: I48477
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1531-1550 <RE55>
 A/Cross-references: EMBL:U06292; NID:g497162; PIDN:AAA65056.1; PID:g510313
 A/Accession: I48478
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1551-1570 <RE56>
 A/Cross-references: EMBL:U06293; NID:g497163; PIDN:AAA65057.1; PID:g510314
 A/Accession: I48479
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1571-1590 <RE57>
 A/Cross-references: EMBL:U06294; NID:g497164; PIDN:AAA65058.1; PID:g510315
 A/Accession: I48480
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1591-1610 <RE58>
 A/Cross-references: EMBL:U06295; NID:g497165; PIDN:AAA65059.1; PID:g510316
 A/Accession: I48481
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1611-1630 <RE59>
 A/Cross-references: EMBL:U06296; NID:g497166; PIDN:AAA65060.1; PID:g510317
 A/Accession: I48482
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1631-1650 <RE60>
 A/Cross-references: EMBL:U06297; NID:g497167; PIDN:AAA65061.1; PID:g510318
 A/Accession: I48483
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1651-1670 <RE61>
 A/Cross-references: EMBL:U06298; NID:g497168; PIDN:AAA65062.1; PID:g510319
 A/Accession: I48484
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1671-1690 <RE62>
 A/Cross-references: EMBL:U06299; NID:g497169; PIDN:AAA65063.1; PID:g510320
 A/Accession: I48485
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1691-1710 <RE63>
 A/Cross-references: EMBL:U06300; NID:g497170; PIDN:AAA65064.1; PID:g510321
 A/Accession: I48486
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1711-1730 <RE64>
 A/Cross-references: EMBL:U06301; NID:g497171; PIDN:AAA65065.1; PID:g510322
 A/Accession: I48487
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1731-1750 <RE65>
 A/Cross-references: EMBL:U06302; NID:g497172; PIDN:AAA65066.1; PID:g510323
 A/Accession: I48488
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1751-1770 <RE66>
 A/Cross-references: EMBL:U06303; NID:g497173; PIDN:AAA65067.1; PID:g510324
 A/Accession: I48489
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1771-1790 <RE67>
 A/Cross-references: EMBL:U06304; NID:g497174; PIDN:AAA65068.1; PID:g510325
 A/Accession: I48490
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1791-1810 <RE68>
 A/Cross-references: EMBL:U06305; NID:g497175; PIDN:AAA65069.1; PID:g510326
 A/Accession: I48491
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1811-1830 <RE69>
 A/Cross-references: EMBL:U06306; NID:g497176; PIDN:AAA65070.1; PID:g510327
 A/Accession: I48492
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1831-1850 <RE70>
 A/Cross-references: EMBL:U06307; NID:g497177; PIDN:AAA65071.1; PID:g510328
 A/Accession: I48493
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1851-1870 <RE71>
 A/Cross-references: EMBL:U06308; NID:g497178; PIDN:AAA65072.1; PID:g510329
 A/Accession: I48494
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1871-1890 <RE72>
 A/Cross-references: EMBL:U06309; NID:g497179; PIDN:AAA65073.1; PID:g510330
 A/Accession: I48495
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1891-1910 <RE73>
 A/Cross-references: EMBL:U06310; NID:g497180; PIDN:AAA65074.1; PID:g510331
 A/Accession: I48496
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1911-1930 <RE74>
 A/Cross-references: EMBL:U06311; NID:g497181; PIDN:AAA65075.1; PID:g510332
 A/Accession: I48497
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1931-1950 <RE75>
 A/Cross-references: EMBL:U06312; NID:g497182; PIDN:AAA65076.1; PID:g510333
 A/Accession: I48498
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1951-1970 <RE76>
 A/Cross-references: EMBL:U06313; NID:g497183; PIDN:AAA65077.1; PID:g510334
 A/Accession: I48499
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1971-1990 <RE77>
 A/Cross-references: EMBL:U06314; NID:g497184; PIDN:AAA65078.1; PID:g510335
 A/Accession: I48500
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1991-2010 <RE78>
 A/Cross-references: EMBL:U06315; NID:g497185; PIDN:AAA65079.1; PID:g510336
 A/Accession: I48501
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2011-2030 <RE79>
 A/Cross-references: EMBL:U06316; NID:g497186; PIDN:AAA65080.1; PID:g510337
 A/Accession: I48502
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2031-2050 <RE80>
 A/Cross-references: EMBL:U06317; NID:g497187; PIDN:AAA65081.1; PID:g510338
 A/Accession: I48503
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2051-2070 <RE81>
 A/Cross-references: EMBL:U06318; NID:g497188; PIDN:AAA65082.1; PID:g510339
 A/Accession: I48504
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2071-2090 <RE82>
 A/Cross-references: EMBL:U06319; NID:g497189; PIDN:AAA65083.1; PID:g510340
 A/Accession: I48505
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2091-2110 <RE83>
 A/Cross-references: EMBL:U06320; NID:g497190; PIDN:AAA65084.1; PID:g510341
 A/Accession: I48506
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2111-2130 <RE84>
 A/Cross-references: EMBL:U06321; NID:g497191; PIDN:AAA65085.1; PID:g510342
 A/Accession: I48507
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2131-2150 <RE85>
 A/Cross-references: EMBL:U06322; NID:g497192; PIDN:AAA65086.1; PID:g510343
 A/Accession: I48508
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2151-2170 <RE86>
 A/Cross-references: EMBL:U06323; NID:g497193; PIDN:AAA65087.1; PID:g510344
 A/Accession: I48509
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2171-2190 <RE87>
 A/Cross-references: EMBL:U06324; NID:g497194; PIDN:AAA65088.1; PID:g510345
 A/Accession: I48510
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2191-2210 <RE88>
 A/Cross-references: EMBL:U06325; NID:g497195; PIDN:AAA65089.1; PID:g510346
 A/Accession: I48511
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 2211-2230 <RE89>
 A/Cross-references: EMBL:

	Query Match	15.5%	Score 186.5	DB 2	Length 560
	Best Local Similarity	28.7%	Pred. No. 5,7e-08		
	Matches	56	Conservative	38	Mismatches 88; Indels 13; Gaps 8;
Oy	1 VPCVSGGLP-KPANTFLSLNNKNVLQWTPPEGLGVK-VITYVOYFIYGKKMLNKSEC	58			
Db	19 LPAASGEANLPENVEIHIIIDNPFLLKAN--SSSESVKVATFSAADYQILGTDMNQKLSGC	76			
Oy	59 RNIRTYCDLDA-ETSDVEHQYAAVKRWGKSKMAESGRFYFLTOTGGPREVALTT	117			
Db	77 QHISTCKNFSSVELENVFKELELRABEGNTSTWEVEBPVDFLAQIGPPVHLIA	136			
Oy	118 DEKSISVVLTAPAEKKRNRPEDLPVSMOOIYSNLKXTNVS-LNTXSNRTMSQCVTHTLVL	176			
Db	137 EDKAIIILISIPP---GTKDSIMMAMDR--SSFRRSVVIWMKSSSLBERTETVPEDKIT	190			
Oy	177 TWLEPNLTLCYHAVES 191				
Db	191 K-LSPEITLYCLAKVKA 204				

RESULT 5

interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C:Accession: A32694; S17112
R:Uze, G.; Lutfailla, G.; Gresser, I.
Cell 60, 223-234, 1990
A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse cell
A:Reference number: A32694; MUID:90124632; PMID:2153461
A:Accession: A32694
A:Molecule type: mRNA
A:Residues: 1-557 <UNZ>
A:Cross-references: UNIPROT:P17181; GB:J03171; NID:9184645; PIDN:AAA52730.1; PID:g306914
R:Lutfailla, G.
submitted to the EMBL Data Library, July 1991
A:Description: The structure of the human interferon alpha/beta receptor gene.
A:Reference number: S17112
A:Accession: S17112
A:Molecule type: DNA
A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>
A:Cross-references: EMBL:X60459; NID:g32671
C:Genetics:
A:Gene: GDB:IFNAR1; IFNAR; IFRC
A:Cross-references: GDB:120078; OMIM:107450
A:Map position: 21q22.1-21q22.1
A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-31/Domain: transmembrane #status predicted <TRN1>
F:437-455/Domain: transmembrane #status predicted <TRN2>
F:50, 58, 81, 88, 110, 172, 254, 313, 314, 376, 415, 433, 507, 518, 537/Binding site: carbohydrate (NA

	Query Match	14.0%;	Score 168.5;	DB 2;	Length 557;
	Best Local Similarity	26.4%;	Pred. No. 1.9e-06;		
	Matches	51;	Conservative	35;	Mismatches 88; Indels 19; Gaps 6;
QY	5	SGG--LKPANITELSLNMKRVLTMPPEGLGVKVTVVQVFYFGKKMKMLNKSECRNIN	62		
Db	25	AGGNLNLSPKVEVDIIDDNFILMNRSDSVG-NVTFSFDYQKGMDMNVIKISGGCNIIT	83		
QY	63	RTYDDLSAERSDYEHQYYAKKAIWGTCKGSMASSGRFYPLETQTIDPPEALTTDEKSI	122		
Db	84	STKNFSSLKLNVYEIKLRIRA-EKENTSSMYVDSTPRRQAIGPPEVHLAEBAKAI	142		
QY	123	SVALTAEBKMERNEDIPVSQQIYSNLKYVASVLATNSKNTMSQCVTN-----HTLVLTW	178		
Db	143	VHHSPPGR-----DSVMMALDGLSPFTSYLLIMNSSGVERLENIYSRHKIHK--	191		
QY	179	LKPNTLYCAVES	191		
	192	LSPETTYCLAKYA	204		

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RESULT 6
A31555
interferon gamma receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: A31555
R:Agnet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A:Title: Molecular cloning and expression of the human interferon-gamma receptor.
A:Reference number: A31555, MUID:89003065, PMID:2971451
A:Accession: A31555
A:Molecule type: mRNA
A:Residues: 1-489 <ACT>
A:Cross-references: UNIPROT:P15260; GB:J03143; NID:g184650; PIDN:AA52731.1; PID:g306921
C:Genetics:
A:Gene: GDB:IFNGR1; IFNGR
A:Cross-references: GDB:I20688; OMIM:107470
A:Map position: 6q23-6q24
C:Superfamily: interferon gamma receptor
C:Keywords: cytokine receptor; transmembrane protein

Query Match      13.6%; Score 163.5; DB 2; Length 489;
Best Local Similarity 24.8%; Pred. No. 4; 4.2e-05;
Matches 51; Conservative 37; Mismatches 79; Indels 39; Gaps 8;

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2

[illegible]

RESULT 7

interleukin-10 receptor - mouse
C|Species: Mus musculus (house mouse)
C|Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C|Accession: A49667
R|Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A|Title: A receptor for interleukin 10 is related to interferon receptors.
A|Reference number: A49667; MUID:9406855; PMID:8248239
A|Accession: A49667
A|Status: preliminary; translated from GB/EMBL/DBD
A|Molecule type: mRNA
A|Residues: 1-575 <RES>
C|Cross-references: UNIPROT:Q61727; GB:L12120; NID:g437615; PIDN:AAA16156.1; PID:g437615
C|Genetics:
A|Gene: IL10R
C|Superfamily: interleukin-10 receptor IL10R
C|Keywords: cytokine receptor

Query Match 13.2% Score 159; DB 2; Length 575;
Best Local Similarity 26.0%; Pred. No. 1.2e-05;
Matches 56; Conservative 33; Mismatches 100; Indels 32; Gaps 8;

Cy 8 LPRANITFLSINKNVLTPTPEGLGVKVTYTVQFIYGOKMLNKSECRNIRTYCD 67
 ||::||::||::||::||::||::||::||::||::||
Db 26 LPSSSYVMFARFFQHILHWKPDPN-QSESTYYEVALKQYGNSTWMDIHICRKXQALSCD 84

Cy 68 LSASTSDYEHO--YAKVKALMGTCCKSAAGSRFPPLFTQIGPREVALTTDEKSISV 124

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Db      85 LTTFTTLJLHRSYGVYRAVAVDSQYSNNTTT-----ETRTVDVLTITD-----SV 133
QY      125 VLTA-----PEKMKRNEDLPV--SMQOITYSLK--YNSVLTAKNSRNTWSQCVTN 171
Db      134 TLKAMDGIIVGTIHPFR-----PTITPAGDEYGVFKDLRYKYSIRKFSKLKATKRVKO 189
QY      172 HTLVLTLEPNTLYCVHVESFVPGPPRRAPQSEKOCARTLKQD 214
Db      190 ETFTLVIPIGVRKFCVAVLPRLESRIKAKMSEBQCLLITTEQ 232

RESULT 8
156215
Interleukin-10 receptor - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 156215
R:Lin, Y.; Wei, S.H.; Ho, A.S.; de Maal Malfeyt, R.; Moore, K.W.
J. Immunol. 152, 1821-1829, 1994
A:Title: Expression cloning and characterization of a human IL-10 receptor.
A:Reference number: 156215; MUID:94165477; PMID:8120391
A:Accession: 156215
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-578 <RBS>
A:Cross-references: UNIPROT:Q13651; EMBL:U00672; NID:9482802; PIDN:AAA17896.1; PID:94828
C:Genetics:
A:Gene: GDB:IL10R; HTL-10R
A:Cross-references: GDB:330958; OMIM:146933
A:Map position: 11q23.3-1q23.3
C:Superfamily: Interleukin-10 receptor IL10R
C:Keywords: cytokine receptor

Query Match      11.9%; Score 143; DB 2; Length 578;
Best Local Similarity 24.8%; Pred. No. 0.00028;
Matches 53; Conservative 37; Mismatches 94; Indels 30; Gaps 10;

QY      8 LKPNATITPLSINMKVLTQWTPREGLOGVYTYVQYFIYGQKMKNSCRNINRTYCD 67
Db      26 LKPPSPVWFAPFAEPFHILHMTPIPN-QSESTCEVALLRKGISWNSISNCQ-TLSY-D 82
QY      68 LSAETSDYHQ--YAKVKAIVGTCKSKMAESGRFPLETOIGPPEVALTTDEKSI--- 122
Db      83 LTAVTLDLHNSNGYRARVRAVDSRSRHSNMTVT-----NTRPSVDEVTLLVGSVMLEIH 135
QY      123 -----SVVLTAEKKMKRNEDLPVSMQOITYSLK--YNSVLTAKNSRNTWSQCVTNT-- 173
Db      136 NGRTILGKIQLPRKMAPAND-----TYESIFSHFREYSLAIRKVPGNFTTHKKVXHEMF 190
QY      174 LVLTWLEPNTLYCVHVESFVPGPPRRAPQSEKOC 207
Db      191 SLTSGEVBG-FCVQVKPSVASRSNKGMSKEEC 223

RESULT 9
156215
Interferon gamma receptor beta subunit - mouse
N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I
C:Species: Mus musculus (house mouse)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49947
R:Hemmli, S.; Bohml, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A:Title: A novel member of the interferon receptor family complements functionality of t
A:Reference number: A49947; MUID:94170381; PMID:8124717
A:Accession: A49947
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-332 <HEM>
A:Cross-references: UNIPROT:Q63953; GB:569336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A:Experimental source: early B-cell line Y16
A>Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)

```

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C:Keywords: cytokine receptor

Query Match      11.5%; Score 138.5; DB 2; Length 332;
Best Local Similarity 23.9%; Pred. No. 0.00034;
Matches 54; Conservative 37; Mismatches 108; Indels 27; Gaps 8;

QY      8 LKPNATITPLSINMKVLTQWTPREGLOGVYTYVQYFIYGQKMKNSCRNINRTY 65
Db      29 LAAFLNPLRLHLNYDEOILTWEPSPSSNDPRVYVQVESFIDGSHRLLRPCTDTETK 88
QY      66 CDLS--AETSDEYHQ--YAKVKAIVGTCKSKMAESGRFPLETOIGPPEVALTTDEKS 121
Db      89 CDLTGGRLKLPFPHPFVFLRVRAKGNLTSKVGLEBFOHYENVTGVPKNIISVTPGKG 148
QY      122 ISVVLTAPEKKMKRNEDLPVSMQOITYSLKVNVSVLTKNSRNTWSQCV-----TNTTLYLT 177
Db      149 SLVHIFSP-----PFD-----VFHGATFQYLHVHWKESLQOQGVGPPKNSIVLG 195
QY      178 WLEPNTLYCVHVESFVPGPPRRAPQ-----SEKOCARTLKQDSEKFK 219
Db      196 NIKPRTVCLQTEAQLILKNKKIRPHGLLSNVSCHETTANMSARLQ 241

RESULT 10
A33368
Interferon gamma receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
C:Accession: A33368; A35468; A34423; A34508; A36224; 148941
R:Kumar, C.S.; Muthukumar, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.; Mariano, T.M.; Pesetka,
J. Biol. Chem. 264, 17939-17946, 1989
A:Title: Molecular characterization of the murine interferon gamma receptor cDNA.
A:Reference number: A33368; MUID:90036866; PMID:2530216
A:Accession: A33368
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <KUN>
A:Cross-references: UNIPROT:P15261; GB:M25764; NID:9197962; PIDN:AAA39177.1; PID:9309393
R:Coifano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Appella, E.
J. Biol. Chem. 265, 4064-4071, 1990
A:Title: Affinity purification, peptide analysis, and cDNA sequence of the mouse interf-
A:Reference number: A35468; MUID:90154099; PMID:2137461
A:Accession: A35468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <COR>
A:Cross-references: GB:J05265; NID:9197964; PIDN:AAA39178.1; PID:9309394
R:Gray, P.W.; Leong, S.; Fennie, E.H.; Farrar, W.A.; Pingel, J.T.; Fernandez-Luna, J.;
Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989
A:Title: Cloning and expression of the cDNA for the murine interferon gamma receptor.
A:Reference number: A34423; MUID:90046824; PMID:2530582
A:Accession: A34423
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94, 'E', '96-477 <GRA>
A:Cross-references: GB:M26711; NID:9194126; PIDN:AAA37896.1; PID:9309330
R:Hemmli, S.; Peghini, P.; Metzler, M.; Merlino, G.; Dembic, Z.; Aguet, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989
A:Title: Cloning of murine interferon gamma receptor cDNA: expression in human cells me
A:Reference number: A34508; MUID:90099370; PMID:2533365
A:Accession: A34508
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94, 'E', '96-477 <HEM>
A:Cross-references: GB:M28233; NID:9194131; PIDN:AAA37898.1; PID:9309331
R:Munro, S.; Maniatis, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
A:Title: Expression cloning of the murine interferon gamma receptor cDNA.
A:Reference number: A36224; MUID:90083245; PMID:2531896
A:Accession: A36224
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 10-477 <MON>

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A:Cross-references: GB:M28995; NID:g194123; PIDN:AAA37895.1; PID:g309329
R:Ravall, P.; Obici, S.; Russell, S.W.; Murphy, W.U.
Gene 154, 219-223, 1995
A>Title: Characterization of the 5' flanking region and gene encoding the mouse interferon
A:Reference number: I48941; MUID:95197006; PMID:7890167
A:Accession: I48941
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <RES>
A:Cross-references: EMBL:U05960; NID:g454092; PIDN:AAA0980.1; PID:g454093
C:Keywords: cytokine receptor; transmembrane protein
Query Match 11.4%; Score 137; DB 2; Length 477;
Best Local Similarity 23.6%; Pred. No. 0.0007;
Matches 55; Conservative 40; Mismatches 98; Indels 40; Gaps 9;
QY 8 LRPKANITFLSINKKVLQMTPEGLQGVK-VTVQVYFYQCKWLNKSECRINRTY 65
DB 38 VDPVITVLTKSYNLNVQWE---YQNSQTFIFVQVQVY-SGSMTD--SCTN1SDHC 90
QY 66 CDLSAETSDYEHQYAKVKAIWGTCCKMAESGRFPFLETOIGPEVAL-TTDEKISIV 124
DB 91 CNITGQIMPDVSAMARVAKVQKESDVAKSEFLMCKLKGKVPGLERKKEQOLSV 150
QY 125 VLTAPKMKRNPEDLPVSNQO-----IYSNLKYNVSVLNTKSNRTSQ 167
DB 151 LVFHPF-----VVVNGESQGMFGDGSCTYPTDYTVVHNHRSGEILHTGTVKEE 202
QY 166 CYNTHLVLTWLEPNTL---YCVHVSFPDGPERRAOPSKQCAITLKQSSSE 217
DB 203 C--NETLCENLISVSTLDSRYCISVDGISSFMQVREKSKDVCIPPHDRKD 253
RESULT 11
138500
Interferon gamma receptor accessory factor-1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C:Accession: I38500; I38501
R:Sch, J.; Donnelly, R.J.; Kosenko, S.; Matiano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.
Cell 76, 793-802, 1994
A>Title: Identification and sequence of an accessory factor required for activation of
A:Reference number: A49946; MUID:94170380; PMID:8124716
A:Accession: I38500
A:Molecule type: mRNA
A:Residues: 1-337 <RES>
A:Cross-references: UNIPROT:P38484; EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g4635
A:Experimental source: clone pSK1
A:Accession: I38501
A:Molecule type: mRNA
A:Residues: 1-63; 'Q', 65-337 <RES>
A:Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
A:Experimental source: clone pJS3
C:Genetics:
A:Map position: 21
C:Keywords: cytokine receptor
Query Match 11.4%; Score 136.5; DB 2; Length 337;
Best Local Similarity 22.5%; Pred. No. 0.00051;
Matches 54; Conservative 33; Mismatches 102; Indels 51; Gaps 11;
QY 8 LRPKANITFLSINKKVLQMTPEGLQGVK-VTVQVYFYQCKWLNKSECRINRTY 60
DB 30 LRPQHPKRLNAEYVLSMEPVALSNSTRPVVYRQ-EKTYDSKFTADINSIGVNCQ 88
QY 61 INRTYCDLSAETSD---YEHQYAKVKAIWGTCCKMAESGRFPFLETOIGPEP-VVL 115
DB 89 IYATECDPFAASPSAGPMDPNTVTLRLRALGLAHSAWMTWPFQHYRVNTVGPENIEV 148
QY 116 TTDEKISIVVLTAP-----EKMKRNPEDLPVSNQOQYISNLKYN-VAVLNT 159
DB 149 TGEBSGLIIRFSSPFDIADTSTAFCYVYVHWEKG-----GIQVQKGPFRSNSISLDNL 202

QY 160 KSNRTWSQCVTNTLVTWLEPNTLYCVHVSFVPGPERRAOPSEKQCAITLKQSSSEFK 219
DB 203 KPSRYV--CLQVQACL-LWKSNIIFRVGHL-----SNISCYETMADASTELQ 246
RESULT 12
KPFH03
tissue factor precursor [validated] - human
N:Alternate names: coagulation factor III
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A43645; A47574; A28320; A29062; A29672; A29008
R:Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1755-1762, 1989
A>Title: Complete sequence of the human tissue factor gene, a highly regulated cellular
A:Reference number: A43645; MUID:89247359; PMID:2719931
A:Accession: A43645
A:Molecule type: DNA
A:Residues: 1-295 <ACT>
A:Cross-references: UNIPROT:P13726; GB:J02846; NID:g339505; PIDN:AAA61152.1; PID:g33950
R:Fishar, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.
Thromb. Res. 48, 89-99, 1987
A>Title: Cloning and expression of human tissue factor cDNA.
A:Reference number: A47574; MUID:88100453; PMID:3424286
A:Accession: A47574
A:Molecule type: mRNA
A:Residues: 1-295 <PIS>
A:Cross-references: GB:M27436; NID:g339507; PIDN:AAA6734.1; PID:g339508
R:Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; L
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
A>Title: Isolation of cDNA clones coding for human tissue factor: primary structure of
A:Reference number: A94171; MUID:87260946; PMID:3037536
A:Accession: A28320
A:Molecule type: mRNA
A:Residues: 1-295 <SPI>
A:Cross-references: GB:U02931; NID:g339501; PIDN:AAA61150.1; PID:g339502
R:Morrissey, J.H.; Fakhral, H.; Edgington, T.S.
Cell 50, 129-135, 1987
A>Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the
A:Reference number: A29062; MUID:87244317; PMID:3297348
A:Accession: A29062
A:Molecule type: mRNA
A:Residues: 1-295 <MOR>
A:Cross-references: GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:g339502
A:Note: part of this sequence, including the amino end of the mature protein, was confi.
R:Scapaty, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Plaudermeyer, R.R.; Siegel,
Biochemistry 26, 5234-5238, 1987
A>Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.
A:Reference number: A29672; MUID:88050796; PMID:2823875
A:Accession: A29672
A:Molecule type: mRNA
A:Residues: 1-259; 'A', 261-295 <SCA>
A:Cross-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
R:Bach, R.; Konigsberg, W.H.; Nemerson, Y.
Biochemistry 27, 4227-4231, 1988
A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cy
A:Reference number: A37422; MUID:89000604; PMID:3166878
A:Content: annotation, disulfide bonds and fatty acid binding site
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C:Comment: Expression of tissue factor can be induced in a variety of tissues by certai
C:Genetics:
A:Gene: GDB:P3
A:Cross-references: GDB:119895; OMIM:134390
A:Map position: 1p22-1p21
A:Intons: 34/1, 71/2, 138/1, 197/3, 251/1
C:Superfamily: tissue factor
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thioester bond; transmembrane
F:1-32/Domain: signal sequence #status predicted <Sig>
F:33-395/Product: tissue factor #status experimental <Mat>
F:33-251/Domain: extracellular #status predicted <Ext>
F:552-274/Domain: transmembrane #status predicted <TM>
F:275-295/Domain: intracellular #status predicted <Int>

F/43/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/91-89,218-241/Disulfide bonds: #status experimental
F/156,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/277/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 11.3%; Score 135.5; DB 1; Length 295;

Best Local Similarity 24.8%; Pred. No. 0.00053;

Matches 55; Conservative 40; Mismatches 98; Indels 29; Gaps 11;

13 NTFSLINMKNVLTQTPPEGLQGVKTYTYQYFYIGQKKMLKSGCRNINRYCDLSAE 71

43 NLTKWSTNFKTILEMPP---KPVNOYTVQ---ISTKSGDWKSKCFYTTDECDLTDSEI 95

72 TSDYEHQYAKVAKIWTGCKSKMAESG-----RPYPLETQIPPEVALTTDEKSI 123

96 VADVQGTIARVSYRAGNVSTGSGEPYKSPPTFLFNLTQPTIQ-SFEQVGRK 154

124 VVLTAPEK--WRNPEDLPVSMQOITY-SNLKYNVSLNTRWSQCVNHTLVLTWL 179

155 VNVTVDERTLVRNNNTFL--SLRDYFGKDLIYTLKYMSSSGK-KTAKTINTEFLIDV 211

180 EPPVLYCVHVESVPPGP--RRAQPEKQCARLTKDQSSFRK 219

212 DKGENYCFVQAVIPRTVNRKSTDSPEVC--MGQEKSEFR 250

Db

RESULT 13

KFMS3

tissue factor precursor - mouse

N/Alternate names: coagulation factor III

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: A32318; A39046

R/Hartzell, S.; Ryder, K.; Ianahan, A.; Lau, L.F.; Nathans, D.

Mol. Cell. Biol. 9, 2567-2573, 1989

A/Title: A growth factor-responsive gene of murine BA16/c 3T3 cells encodes a protein ho

A/Reference number: A32318; MUID:8943974; PMID:2761539

A/Accession: A32318

A/Molecule type: mRNA

A/Residues: 1-294 <HAR>

A/Cross-references: UNIPROT:P20352; GB:M26071; NID:g201924; PIDN:AAA4014.1; PID:g201925

R/Ranganathan, G.; Blatci, S.F.; Subramaniam, M.; Faas, D.N.; Mainhe, N.J.; Getz, M.J.

J. Biol. Chem. 266, 496-501, 1991

A/Title: Cloning of murine tissue factor and regulation of gene expression by transfor

A/Reference number: A39046; MUID:91093171; PMID:1985911

A/Accession: A39046

A/Molecule type: mRNA

A/Residues: 1-25; 1-27-294 <RAN>

A/Cross-references: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927

A/Note: 26-Thr was also found

C/Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor

C/Comment: Expression of tissue factor can be induced in a variety of tissues by certain

C/Superfamily: tissue factor

C/Keywords: blood coagulation; glycoprotein; lipoprotein; cholesterol bond; transmembrane

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-294/Product: tissue factor #status predicted <MAT>

F/252-274/Domain: extracellular #status predicted <EXT>

F/37-57,169,200/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/75-83,218-241/Disulfide bonds: #status predicted

F/275/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 11.0%; Score 131.5; DB 1; Length 294;

Best Local Similarity 25.1%; Pred. No. 0.0011;

Matches 54; Conservative 38; Mismatches 76; Indels 47; Gaps 13;

7 GLPKPA-NITFLSINMKNVLTQTPPEGLQGVKTYTYQYFYIGQKKMLKSGCRNINRY 65

30 GIPEKAFNLTLWISTDEKTLIEMQP---KPTNYTVQ--ISDRSRWKKK--CFSTTDTE 82

66 CDLSAE-TSDYEHQYAKVAKV-----IWGKCKMAESGRFYPLETQIG 109

83 CDLTDEIVKDVWYAEKAVLSVPRNSVHGDDQDLVHGEE--PFTNAPRFLPYRDTNIG 141

Db

QY 110 PEEV-ALTTDEKISV-----LTAPKWRNPEDLPVSMQOITY-SNLKYNV-----SVL 158

Db 142 QPVIQFQEDGKKNLVVVKDSTLTVRK-----NGFPLTRQVFGKDLGIIITRKGSSTG 196

QY 159 TKSNTWSQCVNHTLVLTWLEPNTLYCVHVESFV 193

Db 197 KKTN-----ITNTNEPSIDVEGVSYCFVQAMI 225

Db

RESULT 14

KFER3

tissue factor precursor - rabbit

N/Alternate names: coagulation factor III

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: J00441; S23681

C/Andrews, B.S.; Rehentulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.

Gene 98, 265-269, 1991

A/Title: Conservation of tissue factor primary sequence among three mammalian species.

A/Reference number: J00441; MUID:91200676; PMID:1840552

A/Accession: J00441

A/Molecule type: mRNA

A/Residues: 1-292 <AND>

A/Cross-references: UNIPROT:P24055; GB:M55390; NID:g165696; PIDN:AAA63469.1; PID:g165697

R/Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.

Thromb. Haemost. 66, 315-320, 1991

A/Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis

A/Reference number: S23681; MUID:92081032; PMID:1746002

A/Accession: S23681

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 33-292 <PAW>

A/Cross-references: EMBL:X53521; NID:g1495; PIDN:CAA37597.1; PID:g3980170

C/Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor

C/Comment: Expression of tissue factor can be induced in a variety of tissues by certain

C/Superfamily: tissue factor

C/Keywords: blood coagulation; glycoprotein; lipoprotein; cholesterol bond; transmembrane

F/1-37/Domain: signal sequence #status predicted <SIG>

F/33-292/Product: tissue factor #status predicted <MAT>

F/33-249/Domain: extracellular #status predicted <EXT>

F/250-271/Domain: transmembrane #status predicted <TMM>

F/272-292/Domain: intracellular #status predicted <INT>

F/11,114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/79-87,216-239/Disulfide bonds: #status predicted

F/274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 10.8%; Score 130; DB 1; Length 292;

Best Local Similarity 22.5%; Pred. No. 0.0015;

Matches 51; Conservative 39; Mismatches 89; Indels 48; Gaps 9;

13 NTFSLINMKNVLTQTPPEGLQGVKTYTYQYFYIGQKKMLKSGCRNINRYCDLSAE 71

41 NLTKWSTNFKTILEMPP---KSIDHYTVQ--ISTRLNWN--KSKCFLTAETECULTDEV 93

72 TSDYEHQYAKVAKIWTGCKS-----KMAESGRFYPLETQIGPEVALTTDEKSI 123

94 VADVQGTIARVSYRAGNVSTGSGEPYKSPPTFLFNLTQPTIQ-SFEQVGRK 143

124 VVLTAPEKWRNPEDLPVSMQOITYSNLKYNVSLNTRWSQCVNHTLVLTWL 167

144 -----QSFQVGTXTLVTDARTLVRRNGTFLSLRAVFGKDLNLTLYYRASSTGKKT 197

168 CYTNHTVLTLWLEPNTLYCVHVESVPPPPRAQSEKQARTLKQ 214

198 ATTNTNEFLIDVKGENTCFVQAVIPSKRRKQRPESLTCTSESQ 244

Db

RESULT 15

KFER3

tissue factor precursor - bovine

N/Alternate names: coagulation factor III

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2005, 02:23:48 ; Search time 118.257 Seconds
(without alignments)
663.913 Million cell updates/sec

Title: US-09-745-792A-15

Perfect score: 1080

Sequence: 1 DEVAIIIPAPGNLSVLSTNMK.....GRYSAPSGTECEVGEAIP 203

Scoring table: BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1080	100.0	203	4 AAB85271	Abb85271 Human IL-
2	1080	100.0	203	5 ABG67202	Abg67202 Human int
3	1080	100.0	203	5 AAE23356	Aae23356 Human int
4	1080	100.0	203	5 AAE29065	Aae29065 Human IL-
5	1080	100.0	203	8 ADJ83295	Adj83295 Human int
6	1080	100.0	311	2 AAY41736	Aay41736 Human PRO
7	1080	100.0	311	3 AAY66676	Aay66676 Membrane-
8	1080	100.0	311	3 AAB33440	Aab33440 Human PRO
9	1080	100.0	311	3 AAY44664	Aay44664 Interfero
10	1080	100.0	311	3 AAB44292	Ab444292 Human PRO
11	1080	100.0	311	3 AAY97046	Aay97046 Human TAN
12	1080	100.0	311	4 AAU12187	Aau12187 Human PRO
13	1080	100.0	311	4 AAB85270	Aab85270 Human IL-
14	1080	100.0	311	4 AAE00339	Aae00339 Human cyt
15	1080	100.0	311	4 AAU04059	Aau04059 Human int
16	1080	100.0	311	4 AAB65199	Ab65199 Human PRO
17	1080	100.0	311	5 AAB67201	Ab67201 Human int
18	1080	100.0	311	5 ABB90182	Abb90182 Human pol
19	1080	100.0	311	5 AAE23355	Aae23355 Human int
20	1080	100.0	311	5 ABB84877	Abb84877 Human PRO
21	1080	100.0	311	5 AAE29064	Aae29064 Human IL-
22	1080	100.0	311	5 ABB95483	Abb95483 Human ang
23	1080	100.0	311	6 ABUS8014	Abus8014 Human PRO
24	1080	100.0	311	6 ABUS0922	Abus0922 Novel hum
25	1080	100.0	311	6 ABUS2604	Abus2604 Human sec

26	1080	100.0	311	6 ABO17631	Ab017631 Novel hum
27	1080	100.0	311	6 ABUS60523	Abu60523 Human sec
28	1080	100.0	311	6 ABO25238	Ab025238 Novel hum
29	1080	100.0	311	6 ABUS13905	Abu13905 Human PRO
30	1080	100.0	311	6 ABUS08885	Abu08885 Human PRO
31	1080	100.0	311	6 ABUS72244	Abu72244 Novel hum
32	1080	100.0	311	6 ABUS72490	Abu72490 Novel hum
33	1080	100.0	311	6 ABUS65885	Abu65885 Human PRO
34	1080	100.0	311	6 ABUS4924	Abu4924 Human sec
35	1080	100.0	311	6 ABUS9666	Abu9666 Novel sec
36	1080	100.0	311	6 ABUS61122	Abu61122 Human PRO
37	1080	100.0	311	6 ABUS9239	Abu9239 Human sec
38	1080	100.0	311	6 ABO25936	Ab025936 Human PRO
39	1080	100.0	311	6 ABO24856	Ab024856 Human sec
40	1080	100.0	311	6 ABUS0391	Abu0391 Human sec
41	1080	100.0	311	6 ABUS8945	Abu8945 Human sec
42	1080	100.0	311	6 ABUS92323	Abu92323 Novel hum
43	1080	100.0	311	6 ABUS9388	Abu9388 Novel hum
44	1080	100.0	311	6 ABUS6861	Abu6861 Human sec
45	1080	100.0	311	6 ABUS75853	Abu75853 Human cla

ALIGNMENTS

RESULT 1
AAB85271
ID AAB85271 standard; protein; 203 AA.

AC AAB85271;
XX
XX 07-SBP-2001 (first entry)
XX
DE Human IL-20 receptor subunit IL-20RB extracellular domain fragment.
XX
XX Interleukin 20; IL-20; IL-20RA; ZCYTOR7; IL-20RB; DIRS1; immunoglobulin;
KW antiinflammatory; antiproliferic; antiaesthetic; antibacterial; human;
KM dermatological; antitumor; antagonist.
XX
OS Homo sapiens.
XX
XX WO200146232-A2.
XX
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000MO-US035307.
XX
XX 23-DEC-1999; 99US-00471774.
XX
XX 22-JUN-2000; 2000US-0213416P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
PI Rixon MW, Preenell SR, Fox BA;
PT WPI; 2001-398320/42.
XX
XX Isolated interleukin 20 soluble receptor comprising two polypeptide
PT subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
PT treating inflammatory diseases such as psoriasis.
XX
XX Claim 1; Page 69; 11pp; English.
XX
XX The invention relates to an interleukin 20 (IL-20) soluble receptor
CC comprising two polypeptide subunits IL-20RA (formerly known as ZCYTOR7)
CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably
CC linked together. In one embodiment, one subunit is fused to the constant
CC region of the light chain of an immunoglobulin, and the other subunit is
CC fused to constant region of the heavy chain of an immunoglobulin. The
CC light chain and the heavy chain are connected via a disulfide bond. The
CC soluble receptor can be used to down-regulate IL-20 and thus treat
CC inflammatory diseases such as psoriasis, inflammatory lung injury such as
CC asthma or bronchitis, adult respiratory disease (ARD), septic shock,

CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact
CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and
CC Crohn's disease. The present sequence represents a human IL-20 receptor
CC subunit IL-20RB extracellular domain fragment
XX

Sequence 203 AA;

Query Match 100.0%; Score 1080; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.1e-109;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVALIPAPQNLSTVSTNMKLLMWSPIAPGETVYVSVEYQGEYESLYTSHIMIPSSWC 60
DB 1 DEVALIPAPQNLSTVSTNMKLLMWSPIAPGETVYVSVEYQGEYESLYTSHIMIPSSWC 60
QY 61 SLTGEPCDVDDITATVPYNLRVATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
DB 61 SLTGEPCDVDDITATVPYNLRVATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
QY 121 FHLVLELDLGPQFEFLVAWRRBPGABEHVKNVSGSIPVHLETMERGAAYCVKQTFV 180
DB 121 FHLVLELDLGPQFEFLVAWRRBPGABEHVKNVSGSIPVHLETMERGAAYCVKQTFV 180
QY 181 KAIGRYSAFSQTECEVQGEAIP 203
DB 181 KAIGRYSAFSQTECEVQGEAIP 203

RESULT 2
ABG67202
ID ABG67202 standard; protein; 203 AA.
AC ABG67202;
XX
XX 24-SEP-2002 (first entry)
XX
XX

Human interleukin-20 sub-unit IL20RB extracellular domain protein #1.
XX
XX

IL-20; interleukin-8; IL-8; Chemokine;
neutrophil; monocyte; basophil; eosinophil; chemotacticant; psoriasis;
periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis;
angiogenesis-dependent chronic inflammatory condition; lung cancer;
melanoma; inflammatory disease; diabetes; arteriosclerosis; catarract;
reperfusion injury; cancer; meningitis; rheumatic disease; skin disease;
idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis;
ulcerative colitis; eczema; atopic dermatitis; contact dermatitis;
inflammatory lung disease; ARD; adult respiratory disease; asthma;
bronchitis; pneumonia.

Homo sapiens.

US2002042366-A1.

11-APR-2002.

22-DEC-2000; 2000US-00746359.

23-DEC-1999; 99US-0171969P.

22-JUN-2000; 2000US-0213341P.

XX (THOM/) THOMPSON P.
XX (POST/) FOSTER D C.
XX (XUWV/) XU W.
XX (MADD/) MADDEN K L.
XX (KEL/) KELLY J D.
XX (SPRE/) SPRECHER C A.
XX (BLUM/) BLUMBERG H.
XX (EAGN/) EAGAN M A.
XX (JASP/) JASPERS S R.
XX (CHAN/) CHANDRASEKHAR Y A.
XX (NOVA/) NOVAK J E.
PI Thompson P, Foster DC, Xu W, Madden KJ, Kelly JD, Sprecher CA;

PI Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;
XX WPI; 2002-507215/54.
XX

Treating inflammatory skin and lung diseases using antibodies against
PT interleukins (IL)-20 (which indirectly modulates activation of IL-8),
XX useful for treating e.g. psoriasis, asthma and bronchitis.
XX

Example 2; Page 24; 68pp; English.

The invention describes a method (I) for treating a mammal afflicted with
CC a disease in which an interleukin-20 (IL-20) polypeptide plays a role
CC comprising administering an antagonist of the IL-20 polypeptide to the
CC individual. An important cytokine in the inflammatory process is
CC interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils
CC via chemotaxis and the release of granule enzymes. IL-8 binds to
CC receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is
CC a potent chemottractant for neutrophils, and the early stages of
CC periodontal disease are characterized by the influx of neutrophils. IL-8
CC is a potent inducer of angiogenesis in several angiogenesis-dependent
CC chronic inflammatory conditions, including rheumatoid arthritis,
CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an
CC important source of angiogenic activity in human lung cancer. Also, IL-8
CC expression correlates with experimental metastatic activity of some
CC melanoma cell lines. Therefore an effective method to treat inflammatory
CC diseases would be to administer an agent that would inhibit IL-8. It has
CC been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20
CC can be used to treat these diseases. The method is used for treating
CC diseases in which the IL-20 polypeptide plays a role e.g. inflammatory
CC diseases including diabetes, arteriosclerosis, catarract, reperfusion
CC injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary
CC fibrosis, inflammatory bowel disease (ulcerative colitis), skin disease
CC (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an
CC inflammatory lung disease (adult respiratory disease (ARD), asthma,
CC bronchitis and pneumonia). This sequence represents a human interleukin-
XX 20 (IL-20) polypeptide used in developing the method of the invention

Sequence 203 AA;

Query Match 100.0%; Score 1080; DB 5; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.1e-109;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVALIPAPQNLSTVSTNMKLLMWSPIAPGETVYVSVEYQGEYESLYTSHIMIPSSWC 60
DB 1 DEVALIPAPQNLSTVSTNMKLLMWSPIAPGETVYVSVEYQGEYESLYTSHIMIPSSWC 60
QY 61 SLTGEPCDVDDITATVPYNLRVATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
DB 61 SLTGEPCDVDDITATVPYNLRVATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
QY 121 FHLVLELDLGPQFEFLVAWRRBPGABEHVKNVSGSIPVHLETMERGAAYCVKQTFV 180
DB 121 FHLVLELDLGPQFEFLVAWRRBPGABEHVKNVSGSIPVHLETMERGAAYCVKQTFV 180
QY 181 KAIGRYSAFSQTECEVQGEAIP 203
DB 181 KAIGRYSAFSQTECEVQGEAIP 203

RESULT 3
AAE23356
ID AAE23356 standard; protein; 203 AA.
AC AAE23356;
XX
XX 27-AUG-2002 (first entry)
XX
XX

Human interleukin-20 receptor beta variant (V-IL-20RB) EC domain.
XX
XX

Human, interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA;
XX interleukin-20 receptor beta; IL-20RB; inflammation; arteriosclerosis;
XX diabetes; reperfusion injury; cancer; infectious meningitis; catarract;
XX

KM rheumatoid arthritis; rheumatic fever; systemic lupus erythematosus;
KM antibacterial; cytostatic; dermatological; ophthalmological; vasotropic;
KW variant.
OS Homo sapiens.
OS Synthetic.
PN WO200222153-A2.
XX
XX 21-MAR-2002.
PD
PF 13-SEP-2001; 2001MO-US026557.
XX
XX 15-SEP-2000; 2000US-0233305P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
PI Chandrasekher YA, Jaepers SR;
XX
XX WPI; 2002-425815/45.
DR
DR N-PSDB; AAD37555.
XX
XX
PS Disclosure; Page 51-52; 80pp; English.
XX
XX The present invention relates to a method of down-regulating interleukin
CC (IL)-19. The method involves administration of a polypeptide comprised of
CC the extracellular domain of interleukin-20 receptor alpha (IL-20RA) and
CC the extracellular domain of interleukin-20 receptor beta (IL-20RB). The
CC IL-20RA and IL-20RB are heterodimeric receptors that bind to both IL-19
CC and mda. The method is useful for down-regulating IL-19, useful for the
CC treatment of inflammation e.g., in diabetes, atherosclerosis, cataracts,
CC reperfusion injury, cancer, infectious meningitis, rheumatoid arthritis,
CC rheumatic fever and systemic lupus erythematosus. The present sequence is
CC human IL-20RB extracellular domain protein
XX
XX
SQ Sequence 203 AA;

Query Match 100.0%; Score 1080; DB 5; Length 203;
Best Local Similarity 100.0%; Pred. No. 5, 1e-109;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVAIIIPAPQNLSTVLTNNKHLMSPVLAPEGTVVYVYSGEYSLSYTSHTWISSWC 60
DB 1 DEVAIIIPAPQNLSTVLTNNKHLMSPVLAPEGTVVYVYSGEYSLSYTSHTWISSWC 60
QY 61 SLTEGPECVTDITATVPYNLRVRAATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
DB 61 SLTEGPECVTDITATVPYNLRVRAATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
QY 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
DB 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
QY 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
DB 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
QY 181 KALGRYSAFSQTCEVGEAIP 203
DB 181 KALGRYSAFSQTCEVGEAIP 203

RESULT 4
AAE29065
ID AAE29065 standard; protein; 203 AA.
XX
XX AAE29065;
AC
XX
XX 27-JAN-2003 (first entry)
DT
XX
XX Human IL-22RB protein #2.
DE
XX
XX Human; heterodimeric cytokine receptor; interleukin-22R; IL-22R; asthma;
KW

KM inflammatory disease; psoriasis; adult respiratory disease; bronchitis;
KW septic shock; multiple organ failure; inflammatory lung injury; eczema;
KW bacterial pneumonia; dermatitis; ulcerative colitis; Crohn's disease;
KW antiinflammatory; dermatological; antibacterial; immunosuppressive;
KW anticancer; ZcytoR11.
XX
XX Homo sapiens.
OS
OS
PN WO200272607-A2.
XX
XX 19-SEP-2002.
PD
PF 07-MAR-2002; 2002MO-US007214.
XX
XX 09-MAR-2001; 2001US-0274560P.
XX
XX 21-JUN-2001; 2001US-0299865P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
PI Chandrasekher YA, Novak JE, Foster DC, Xu W, Jaepers SR;
XX
XX WPI; 2002-723314/78.
DR
XX
XX
PS Claim 1; Page 59-60; 82pp; English.
XX
XX The present invention relates to novel heterodimeric cytokine receptor
CC which comprises an interleukin-22R (IL-22R; ZcytoR11) subunit. Receptor
CC sequences are useful for down-regulating IL-20 and treating inflammatory
CC diseases such as psoriasis, adult respiratory disease, multiple organ
CC failure, septic shock, inflammatory lung injury such as bronchitis or
CC asthma, bacterial pneumonia, eczema, atopic and contact dermatitis,
CC ulcerative colitis and Crohn's disease. The present sequence is human
CC interleukin-22RB (IL-22RB) protein
XX
XX
SQ Sequence 203 AA;

Query Match 100.0%; Score 1080; DB 5; Length 203;
Best Local Similarity 100.0%; Pred. No. 5, 1e-109;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVAIIIPAPQNLSTVLTNNKHLMSPVLAPEGTVVYVYSGEYSLSYTSHTWISSWC 60
DB 1 DEVAIIIPAPQNLSTVLTNNKHLMSPVLAPEGTVVYVYSGEYSLSYTSHTWISSWC 60
QY 61 SLTEGPECVTDITATVPYNLRVRAATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
DB 61 SLTEGPECVTDITATVPYNLRVRAATLGSQTSAMSLIKHPFNRSSTILTRPGMEITKDG 120
QY 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
DB 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
QY 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
DB 121 FHLVLELDLGPQFEFLVAYWRREPGAEHVKVNRSGGIPVHLETPGGAAYCVKAQTFV 180
QY 181 KALGRYSAFSQTCEVGEAIP 203
DB 181 KALGRYSAFSQTCEVGEAIP 203

RESULT 5
ADJ83295
ID ADJ83295 standard; protein; 203 AA.
XX
XX ADJ83295;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human interleukin receptor IL-20RB extracellular domain mature protein.
DE
XX
XX Inflammation; single chain antibody; interleukin; IL-20; IL-20RA subunit;
KW

KW IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic;
KW antiarthritic; respiratory; antisclerotic; antitumor; antibacterial;
KW immunosuppressive; gastroenteric; skin; psoriasis; eczema;
KW atopic dermatitis; contact dermatitis; lung; pneumonia;
KW adult respiratory distress syndrome; asthma; bronchitis;
KW arthritis; septic shock; multiple organ failure; bowel;
KW ulcerative colitis; Crohn's disease; human; receptor;
KW extracellular domain; mature.
XX
XX Homo sapiens.
XX
XX US2004005320-A1.
XX
XX 08-JAN-2004.
XX
XX 26-APR-2003; 2003US-00424658.
XX
XX 23-DEC-1999; 99US-0171969P.
XX 22-JUN-2000; 2000US-0213341P.
XX 22-DEC-2000; 2000US-00746359.
XX
XX (THOM/) THOMPSON P.
XX (FOST/) FOSTER D C.
XX (XUW/) XU W.
XX (MADD/) MADDEN K L.
XX (KELL/) KELLY J D.
XX (SPRE/) SPRECHER C A.
XX (BLIN/) BLUMBERG H.
XX (BAG/) BAGAN M A.
XX (JASP/) JASPERS S R.
XX (CHAN/) CHANDRASEKHAR Y A.
XX (NOVA/) NOVAK J E.
XX
XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;
PI Blumberg H, Egan MA, Jaspers SR, Chandrasekhar YA, Novak JE;
XX
XX WPI; 2004-081696/08.
XX
XX N-PSDB; ADJ83293.
XX
XX
XX Reducing or treating inflammation, e.g. inflammatory lung disease,
PT comprises administering an antibody, antibody fragment or single chain
PT antibody that specifically binds to an interleukin (IL)-20RA subunit of
PT an IL-20 receptor.
XX
XX
XX Example 2; SEQ ID NO 15; 69pp; English.
XX
XX The invention relates to a novel method of reducing or treating
XX inflammation in a mammal which comprises administering an antibody,
XX antibody fragment or single chain antibody which specifically binds to a
XX receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-
XX 20RB subunit. The method of the invention has antiinflammatory,
XX dermatological, antipsoriatic, antiarthritic, respiratory, antisclethatic,
XX antitumor, antibacterial, immunosuppressive and gastroenteric
XX applications and may be useful for reducing or treating inflammation,
XX including an inflammatory skin disease such as psoriasis, eczema, atopic
XX dermatitis and contact dermatitis or an inflammatory lung disease such as
XX adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as
XX well as arthritis, septic shock, multiple organ failure, inflammatory
XX bowel disease, ulcerative colitis or Crohn's disease. The current
XX sequence is that of the human IL-20RB subunit-related protein of the
XX invention.
XX
XX Sequence 203 AA;
SQ
Query Match 100.0%; Score 1080; DB 8; Length 203;
Best Local Similarity 100.0%; Pred. No. 5,1e-109;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 SLTEGPECVDTDITATVPYNLRVATLGSQTSAMSLKHPFNRSITILTRPGMEITTKDG 120
QY 121 FHLVLELDLGGQFEFLVAYMRREGABEHVMVSGIPVLTETMERGAAYCVAQTFV 180
DB 121 FHLVLELDLGGQFEFLVAYMRREGABEHVMVSGIPVLTETMERGAAYCVAQTFV 180
QY 181 KAIGRYSAFSQTECVVOGEAIP 203
DB 181 KAIGRYSAFSQTECVVOGEAIP 203
RESULT 6
AA41736
ID AA41736 standard; protein; 311 AA.
XX
XX AA41736;
XX
XX 07-DEC-1999 (first entry)
XX
XX Human PRO114 protein sequence.
XX
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
XX Homo sapiens.
XX
XX WO9946281-A2.
XX
XX 16-SEP-1999.
XX
XX 08-MAR-1999; 99WO-US005028.
XX
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 31-MAR-1998; 98US-0080105P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080165P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080328P.
XX 01-APR-1998; 98US-0080333P.
XX 01-APR-1998; 98US-0080334P.
XX 01-APR-1998; 98US-0080349P.
XX 08-APR-1998; 98US-0081034P.
XX 08-APR-1998; 98US-0081070P.
XX 08-APR-1998; 98US-0081071P.
XX 09-APR-1998; 98US-0081195P.
XX 09-APR-1998; 98US-0081203P.
XX 09-APR-1998; 98US-0081229P.
XX 15-APR-1998; 98US-0081817P.
XX 15-APR-1998; 98US-0081838P.
XX 15-APR-1998; 98US-0081952P.
XX 15-APR-1998; 98US-0081955P.
XX 21-APR-1998; 98US-0082568P.

PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082766P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083332P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086466P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 30-MAY-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI, 1999-551358/46.
DR N-PSDB; AA234190.
XX
XX
PT New secreted and transmembrane polypeptides and their polynucleotides.
PT useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.
XX
XX Claim 12; Fig 142; 530P; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AA233891 to AA24338, and AA24185 to
XX AA241774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention

XX SQ Sequence 311 AA;
Query Match 100.0%; Score 1080; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 9, 8e-109;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVAIIIPAPQNLVSLTNMGLHMSVPVAPGETVTVYSVYQGEYESLYSHIWPSSWC 60
DB 30 DEVAIIIPAPQNLVSLTNMGLHMSVPVAPGETVTVYSVYQGEYESLYSHIWPSSWC 89
QY 61 SLTEGPCVDYTDITATVPNLVRATLSQTSAMSLKHPFNRNSTILTRPGMETKDG 120
DB 90 SLTEGPCVDYTDITATVPNLVRATLSQTSAMSLKHPFNRNSTILTRPGMETKDG 149
QY 121 FHLVIELEDGPOPEFLVAYWRREPGAEHEVKKVRSQGI PVHLETMEPGAAYCAKQTFV 180
DB 150 FHLVIELEDGPOPEFLVAYWRREPGAEHEVKKVRSQGI PVHLETMEPGAAYCAKQTFV 209
QY 181 KAIGRYSAFSQTECVVQGEAIP 203
DB 210 KAIGRYSAFSQTECVVQGEAIP 232
RESULT 7
AA26676
ID AA26676 standard; protein; 311 AA.
XX
AC AA26676;
XX
DT 05-APR-2000 (first entry)
XX
XX Membrane-bound protein PRO1114.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIB ligand;
XX KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX OS Homo sapiens.
XX
XX PN WO9963088-A2.
XX
XX PD 09-DEC-1999.
XX
XX PF 02-JUN-1999; 99WO-US012252.
XX
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 02-JUN-1998; 98US-0087759P.
XX PR 03-JUN-1998; 98US-0087827P.
XX PR 04-JUN-1998; 98US-0088021P.
XX PR 04-JUN-1998; 98US-0088025P.
XX PR 04-JUN-1998; 98US-0088028P.
XX PR 04-JUN-1998; 98US-0088029P.
XX PR 04-JUN-1998; 98US-0088030P.
XX PR 04-JUN-1998; 98US-0088033P.
XX PR 04-JUN-1998; 98US-0088326P.
XX PR 05-JUN-1998; 98US-0088167P.
XX PR 05-JUN-1998; 98US-0088202P.
XX PR 05-JUN-1998; 98US-0088212P.
XX PR 05-JUN-1998; 98US-0088217P.
XX PR 05-JUN-1998; 98US-0088255P.
XX PR 09-JUN-1998; 98US-0088722P.
XX PR 10-JUN-1998; 98US-0088730P.
XX PR 10-JUN-1998; 98US-0088734P.
XX PR 10-JUN-1998; 98US-0088738P.
XX PR 10-JUN-1998; 98US-0088740P.
XX PR 10-JUN-1998; 98US-0088741P.
XX PR 10-JUN-1998; 98US-0088742P.
XX PR 10-JUN-1998; 98US-0088810P.
XX PR 10-JUN-1998; 98US-0088811P.
XX PR 10-JUN-1998; 98US-0088824P.
XX PR 10-JUN-1998; 98US-0088825P.
XX PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089050P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089589P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 07-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095311P.
PR 04-AUG-1998; 98US-0095312P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.

PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096849P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,
Wood WT, Yuan J;

WPI; 2000-072883/06.

DR N-PSDB; AA265011.

Membrane-bound proteins and related nucleotide sequences.

Claim 12; Fig 117; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques

XX Sequence 311 AA;

Query Match 100.0%; Score 1080; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 9; 8e-109;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVALPAPQNLSTVSTMKHLLMWSPIVARGETVYVSVEYQGEYESLXTSHWIPSSWC 60
DB 30 DEVALPAPQNLSTVSTMKHLLMWSPIVARGETVYVSVEYQGEYESLXTSHWIPSSWC 89


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QY 61 SLTEGPCDVTDDITATVPYNLRATLGSQTSAMSLIKPFRNNTILTRPGMEITKDG 120
DB 90 SLTEGPCDVTDDITATVPYNLRATLGSQTSAMSLIKPFRNNTILTRPGMEITKDG 149
QY 121 FHLVIELEDGPOPEFLVAYWRREPAGAEHVKVNRSGGIPVHLETMPGAAVCYKAQTFV 180
DB 150 FHLVIELEDGPOPEFLVAYWRREPAGAEHVKVNRSGGIPVHLETMPGAAVCYKAQTFV 209
QY 181 KAIGRYSAFSQTECEVGEAIP 203
DB 210 KAIGRYSAFSQTECEVGEAIP 232

RESULT 8
AAB33440
ID AAB33440 standard; protein; 311 AA.
XX
AC AAB33440;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1114 protein UNQ557 SEQ ID NO:144.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antineumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antiparasitic; antiallergic;
KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW autoimmune thrombocytopenia; autoimmune haemolytic anaemia; diabetes mellitus;
KW demyelinating disease; hepatobiliary disease; immune-mediated renal disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
PN MO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000MO-US005841.
XX
PR 08-MAR-1999; 99MO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99MO-US028849P.
PR 20-APR-1999; 99MO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99MO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99MO-US020111.
PR 08-SEP-1999; 99MO-US020594.
PR 13-SEP-1999; 99MO-US020944.
PR 15-SEP-1999; 99MO-US021090.
PR 15-SEP-1999; 99MO-US021547.
PR 05-OCT-1999; 99MO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99MO-US028214.
PR 30-NOV-1999; 99MO-US028313.
PR 30-NOV-1999; 99MO-US028409.
PR 01-DEC-1999; 99MO-US028301.
PR 01-DEC-1999; 99MO-US028634.
PR 02-DEC-1999; 99MO-US028551.
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PR 02-DEC-1999; 99MO-US028564.
PR 02-DEC-1999; 99MO-US028565.
PR 16-DEC-1999; 99MO-US030095.
PR 20-DEC-1999; 99MO-US030999.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000277.
PR 06-JAN-2000; 2000MO-US000376.
PR 11-FEB-2000; 2000MO-US003565.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
XX
XX (GENENTECH INC.
XX
PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W,
PI Kabakoff RC, Lu Y, Pan Y, Pennica D, Shelton DL, Smith V,
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M,
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58605.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 33; Fig 54; 309pp; English.
```

```
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC anaemia, autoimmune haemolytic anaemia, autoimmune haemolytic
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
```

Sequence 311 AA;

Query Match 100.0%; Score 1080; DB 3; Length 311;

Best Local Similarity 100.0%; Pred. No. 9.8e-109; Indels 0; Gaps 0;

Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 DEVAIIIPAPONTLSVLTNNKHLMSVPIAPGETVYVSYEGEYSLSYTHIMIPSSWC 60
DB 30 DEVAIIIPAPONTLSVLTNNKHLMSVPIAPGETVYVSYEGEYSLSYTHIMIPSSWC 89
QY 61 SLTEGPCDVTDDITATVPYNLRATLGSQTSAMSLIKPFRNNTILTRPGMEITKDG 120
DB 90 SLTEGPCDVTDDITATVPYNLRATLGSQTSAMSLIKPFRNNTILTRPGMEITKDG 149
QY 121 FHLVIELEDGPOPEFLVAYWRREPAGAEHVKVNRSGGIPVHLETMPGAAVCYKAQTFV 180
DB 150 FHLVIELEDGPOPEFLVAYWRREPAGAEHVKVNRSGGIPVHLETMPGAAVCYKAQTFV 209
QY 181 KAIGRYSAFSQTECEVGEAIP 203
DB 210 KAIGRYSAFSQTECEVGEAIP 232
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RESULT 9
AAY44664

ID AAY44664 standard; protein; 311 AA.
XX AAY44664;
XX
XX 18-APR-2000 (first entry)
DE Interferon Receptor-HKAEF92.
XX
KM Interferon receptor HKAEF92; INFR; ATCC No. 209746; viral infection;
KM immune dysfunction; immune system disorder; proliferative disease;
KM cancer; inflammatory disorder; persistent infection; autoimmune disease;
KM arthritis; leukemia; lymphoma; immunosuppression; myelosuppression;
XX inflammatory bowel disease; Jaks-STATs signal transduction pathway.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Signal_peptide
FT Peptide 69..77
FT /note= "Antigenic epitope-bearing peptide"
FT Peptide 92..107
FT /note= "Antigenic epitope-bearing peptide"
FT Peptide 129..162
FT /note= "Antigenic epitope-bearing peptide"
FT Domain 130..233
FT /label= Extracellular_domain
FT Peptide 172..199
FT /note= "Antigenic epitope-bearing peptide"
FT Domain 234..250
FT /label= Transmembrane_domain
FT Domain 251..311
FT /label= Intracellular_domain
FT Peptide 272..307
FT /note= "Antigenic epitope-bearing peptide"
XX
XX WO962934-A1.
XX
XX 09-DEC-1999.
XX
XX 03-JUN-1999; 99WO-US012156.
XX
XX 05-JUN-1998; 98US-0088185P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ni J;
XX
XX WPI; 2000-147043/13.
XX N-PSDB; AAZ49747.
XX
XX New isolated interferon receptor HKAEF92 polynucleotides, used to develop
XX products for treating, e.g. immune system related disorders.
XX
XX Claim 17, Fig 1; 98PP; English.
XX
XX The present sequence is interferon receptor (INFR) HKAEF92 encoded by
XX cDNA clone HKAEF92 (ATCC No. 209746) derived from human keratinocyte cDNA
XX library. INFR-HKAEF92 polypeptides are used in the treatment of disorders
XX associated with viral infection, immune dysfunction and proliferative
XX diseases such as cancer, inflammatory disorders, persistent infection,
XX autoimmune diseases, arthritis, leukemias, lymphomas, immunosuppression,
XX inflammatory bowel disease, or myelosuppression. The products can also be
XX used for detection, diagnosis and drug screening. INFR-HKAEF92 protein
XX activates Jaks-STATs signal transduction pathway in a dose-dependent
XX manner
XX
XX Sequence 311 AA.
XX
XX Query Match 100.0%; Score 1080; DB 3; Length 311;
XX Best Local Similarity 100.0%; Pred. No. 9,8e-109;
XX Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVALIPAPQNLSTLNKHLMSPVIAGETVYVSVEQGEYESTLTSHTWIPSSWC 60
DB 30 DEVALIPAPQNLSTLNKHLMSPVIAGETVYVSVEQGEYESTLTSHTWIPSSWC 89
QY 61 SLTEGPCDVTDDITATVPPNLRVATLGSQTSASMLKHPNNSTLITRPGMEITKDG 120
DB 90 SLTEGPCDVTDDITATVPPNLRVATLGSQTSASMLKHPNNSTLITRPGMEITKDG 149
QY 121 FHLVLELDLGPQFEFLVVMRRPGAEHVMKVSQGI PVHLETMERGAAYCVRQTFV 180
DB 150 FHLVLELDLGPQFEFLVVMRRPGAEHVMKVSQGI PVHLETMERGAAYCVRQTFV 209
QY 181 KAIGRYSAFSQTECVVQGEAIP 203
DB 210 KAIGRYSAFSQTECVVQGEAIP 232
RESULT 10
ID AAB44292 standard; protein; 311 AA.
XX AAB44292;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human PRO1114 (UNQ557) protein sequence SEQ ID NO:352.
XX
XX Human; secreted protein; transmembrane protein; PRO; ESR; cytoslatic;
XX expressed sequence tag; detection; cancer.
XX
XX Homo sapiens.
XX
XX MO200053756-A2.
XX
XX 14-SEP-2000.
XX
XX 18-FEB-2000; 2000WO-US004341.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 98US-0123957P.
XX 29-MAR-1999; 98US-0126773P.
XX 21-APR-1999; 99US-0102323P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 29-OCT-1999; 98US-0162506P.
XX 30-NOV-1999; 99WO-US028513.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US030095.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX
XX (GENTH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
XX Ferrara N, Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,
XX Goddard A, Godowski PJ, Grimaldi CJ, Guirney AL, Hillan KJ,
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
XX Stewart TA, Tumas D, Williams PM, Wood WI,
XX WPI; 2000-611443/58.
XX N-PSDB; AAC78547.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
XX target bioactive molecules to specific cells, and to modulate cellular
XX activities.
XX
XX Claim 12, Fig 142; 636PP; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. CC The PRO polynucleotides and polypeptides have cytostatic activity. The CC polynucleotides and polypeptides can be used for detecting the presence CC of PRO polypeptides in samples, for linking bioactive molecules to cells CC and for modulating biological activities of cells, using the polypeptides CC for specific targeting. The polypeptide targeting can be used to kill the CC target cells, e.g. for the treatment of cancers. The polypeptide pairs CC provide specific targeting of bioactive molecules to cells. AAC78600 to CC AAC78697 represent PCR primers and probes used in the isolation of the CC PRO polynucleotide sequences

XX Sequence 311 AA;

Query Match 100.0%; Score 1080; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.8e-109; Indels 0; Gaps 0;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVAIIPAPONLSVLTNNKMLMSPVIAAGETVYYSVEYQGEYSLYTSHIWPSSWC 60
30 DEVAIIPAPONLSVLTNNKMLMSPVIAAGETVYYSVEYQGEYSLYTSHIWPSSWC 89
QY 61 SLTEGPCDVTDDITATVPYNLRVATLGSQTSAMSILKHPFNNSITILTRPGMEITKDG 120
90 SLTEGPCDVTDDITATVPYNLRVATLGSQTSAMSILKHPFNNSITILTRPGMEITKDG 149
QY 121 FHLVIELBDLGPQEFVLVAYWRREPQAEHVKVNRSGGIPVHLETWEPGAAYCVKAQTFV 180
150 FHLVIELBDLGPQEFVLVAYWRREPQAEHVKVNRSGGIPVHLETWEPGAAYCVKAQTFV 209
Db 181 KAIGRYSAFSQTECVQGEAIP 203
210 KAIGRYSAFSQTECVQGEAIP 232
QY 181 KAIGRYSAFSQTECVQGEAIP 203
210 KAIGRYSAFSQTECVQGEAIP 232
Db 210 KAIGRYSAFSQTECVQGEAIP 232

RESULT 11
AA97046 standard; protein; 311 AA.
XX AA97046;
AC AA97046;
XX
DT 31-OCT-2000. (first entry)
XX
DE Human TANGO 242.
XX
KM TANGO 242; transmembrane, class II; cytokine receptor; chromosome 3q21;
KW cytoskeletal; cerebroprotective; immunomodulatory; anti-inflammatory;
KW vlnucide; antibacterial; vasotropic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..29 /label= Signal_peptide
FT Protein 30..311 /label= Mature_protein
FT Domain 30..230 /label= Extracellular_domain
FT Domain 35..125 /label= Fibronectin_III_domain
FT Modified-site 40 /label= Fibronectin_III_domain
FT Modified-site 134 /note= "N-linked glycosylation site"
FT Modified-site 231..255 /note= "N-linked glycosylation site"
FT Domain 256..311 /label= Transmembrane_domain
FT Domain 256..311 /label= Cytolaemic_domain
PN MO200039161-A1.
XX 06-JUL-2000.
PD

XX 30-DEC-1999; 99WO-US033328.
XX
XX 31-DEC-1998; 98US-00224669.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Busfield SJ;
PI
XX WPI: 2000-452372/39.
DR
DR N-PSDB; AAA51871, AAA51872.
XX
XX New nucleic acid molecules encoding polypeptides designated TANGO 241 and
PT TANGO 242 used for treating e.g. brain and pancreatic disorders.
XX
XX Claim 8; Fig 3; 127pp; English.
PS
XX Novel transmembrane proteins, designated TANGO 241 and TANGO 242, are
CC members of the class II cytokine receptor superfamily. The TANGO 241 and
CC 242 genes have been localized to human chromosomes 1p36 and 3q21,
CC respectively. The proteins, cDNA and their modulators can be used for the
CC treatment of viral and bacterial infection, inflammatory and autoimmune
CC disorders, vascular injury and inhibition of angiogenesis. In particular,
CC TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be
CC used to treat brain disorders

XX Sequence 311 AA;

Query Match 100.0%; Score 1080; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.8e-109; Indels 0; Gaps 0;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVAIIPAPONLSVLTNNKMLMSPVIAAGETVYYSVEYQGEYSLYTSHIWPSSWC 60
30 DEVAIIPAPONLSVLTNNKMLMSPVIAAGETVYYSVEYQGEYSLYTSHIWPSSWC 89
QY 61 SLTEGPCDVTDDITATVPYNLRVATLGSQTSAMSILKHPFNNSITILTRPGMEITKDG 120
90 SLTEGPCDVTDDITATVPYNLRVATLGSQTSAMSILKHPFNNSITILTRPGMEITKDG 149
QY 121 FHLVIELBDLGPQEFVLVAYWRREPQAEHVKVNRSGGIPVHLETWEPGAAYCVKAQTFV 180
150 FHLVIELBDLGPQEFVLVAYWRREPQAEHVKVNRSGGIPVHLETWEPGAAYCVKAQTFV 209
Db 181 KAIGRYSAFSQTECVQGEAIP 203
210 KAIGRYSAFSQTECVQGEAIP 232
QY 181 KAIGRYSAFSQTECVQGEAIP 203
210 KAIGRYSAFSQTECVQGEAIP 232
Db 210 KAIGRYSAFSQTECVQGEAIP 232

RESULT 12
AAU12187 standard; protein; 311 AA.
XX AAU12187;
AC AAU12187;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO114 polypeptide sequence.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumor necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy.
XX
OS Homo sapiens.
XX
OS
XX
PN MO200140466-A2.
XX
XX 07-JUN-2001.
PD
XX 01-DEC-2000; 2000WO-US032678.
XX
XX 01-DEC-1999; 99WO-US028301.
PR

PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
 XX WPI: 2001-408281/43.
 DR N-PSDB; AAS21259.
 XX Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 PS Claim 12; Fig 32; 813pp; English.
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (BMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO

CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 311 AA;
 Query Match 100.0%; Score 1080; DB 4; Length 311;
 Best Local Similarity 100.0%; Pred. No. 9,8e-109;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVALIPAPQNLSTVSTNNKHLIMSPVAPGETYYVYSGEYESLYTSHWIPSSWC 60
 DB 30 DEVALIPAPQNLSTVSTNNKHLIMSPVAPGETYYVYSGEYESLYTSHWIPSSWC 89
 QY 61 SLTEGPCVYTDITATVPYNLRVATIGSOTSANSILKHPNNRSTLLTRPGMEITKDG 120
 DB 90 SLTEGPCVYTDITATVPYNLRVATIGSOTSANSILKHPNNRSTLLTRPGMEITKDG 149
 QY 121 FHLVLELDLGPQFELVAVWRREPABEHVQMRSSGIPVHLEMERGAAYCVKQTFV 180
 DB 150 FHLVLELDLGPQFELVAVWRREPABEHVQMRSSGIPVHLEMERGAAYCVKQTFV 209
 QY 181 KAIGRYSAFSQTECYEVOGEALP 203
 DB 210 KAIGRYSAFSQTECYEVOGEALP 232
 RESULT 13
 AAB85270
 ID AAB85270 Elandard; protein; 311 AA.
 AC AAB85270;
 XX
 DT 07-SBP-2001 (first entry)
 XX
 DE Human IL-20 receptor subunit IL-20RB.
 XX
 KW Interleukin 20; IL-20; IL-20RA; Zcytor7; IL-20RB; DIRS1; immunoglobulin;
 KW antiinflammatory; antipsoriatic; antiaesthetic; antibacterial; human;
 KW dermatological; antitumor; antagonist.
 XX
 OS Homo sapiens.
 XX
 XX WO200146232-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 22-DEC-2000; 2000WO-US035307.
 XX
 XX 23-DEC-1999; 99US-00471774.
 PR 22-JUN-2000; 2000US-0213416P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 PI Foester DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
 PI Rixson MW, Presnell SR, Fox BA;
 DR N-PSDB; AAH22816.
 XX WPI: 2001-398320/42.
 XX
 PT Isolated interleukin 20 soluble receptor comprising two polypeptide
 PT subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
 PT treating inflammatory diseases such as psoriasis.
 XX
 PS Example 2; Page 68-69; 119pp; English.
 XX
 CC The invention relates to an interleukin 20 (IL-20) soluble receptor
 CC comprising two polypeptide subunits IL-20RA (formerly known as Zcytor7)
 CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably
 CC linked together, in one embodiment, one subunit is fused to the constant
 CC region of the light chain of an immunoglobulin, and the other subunit is
 CC fused to constant region of an immunoglobulin. The
 CC light chain and the heavy chain are connected via a disulphide bond. The
 CC soluble receptor can be used to down-regulate IL-20 and thus treat

CC inflammatory diseases such as psoriasis, inflammatory lung injury such as
CC asthma or bronchitis, adult respiratory disease (ARD), septic shock,
CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact
CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and
CC Crohn's disease. The present sequence represents a human IL-20 receptor
CC subunit IL-20RB
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 1080; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.8e-109; Mismatches 0; Gaps 0;
Matches 203; Conservative 0; Indels 0; Gaps 0;

QY 1 DEVAIIIPAPQNLSTLNKMKHLLMSPVIAFGETVYVSEYQGEYSLSYTHIMIPSSWC 60
DB 30 DEVAIIIPAPQNLSTLNKMKHLLMSPVIAFGETVYVSEYQGEYSLSYTHIMIPSSWC 89

QY 61 SLTEGPECDVTDDITATVPNNLRVRAVLGSGTSAMSLIKHPFRNNTILTRPCEMTTKDG 120
DB 90 SLTEGPECDVTDDITATVPNNLRVRAVLGSGTSAMSLIKHPFRNNTILTRPCEMTTKDG 149

QY 121 FHLVIELEDIGPQFEFLVAYMRREPAGAEHVKVNRSGGIPVHLETPMPPGAAYCVKQOTFV 180
DB 150 FHLVIELEDIGPQFEFLVAYMRREPAGAEHVKVNRSGGIPVHLETPMPPGAAYCVKQOTFV 209

QY 181 KAIGRYSAFSQTECEVQGEAIP 203
DB 210 KAIGRYSAFSQTECEVQGEAIP 232

RESULT 14
AAE00339
ID AAE00339 standard; protein; 311 AA.
XX
AC AAE00339;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human cytokine receptor protein, CG92.
XX
KM Human; cytokine receptor protein; CG92; antiinflammatory; antimicrobial;
KM immunosuppressive; blood coagulation disorder; antidiabetic; cytotoxic;
KM gastrointestinal; acute pancreatitis; glomerulonephritis; gene therapy;
KM severe combined immunodeficiency; SCID; autoimmune disorder; thrombosis;
KM multiple sclerosis; rheumatoid arthritis; Alzheimer's disease; xenograft;
KM graft versus host disease; GVHD; inflammatory bowel disease; haemostatic;
KM endotoxin shock; psoriasis; osteoporosis; hepatitis; vascular; allograft;
KM cell proliferative; haematopoietic; vasculitis; lupus; leukaemia; cancer;
KM sarcoidosis; sepsis.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT 1..29 /label= Signal_peptide
FT /label= Signal_peptide
FT 30..311 /label= Mature_human CG92_protein
FT /label= Mature_human CG92_protein
FT 35..224 /note= "Tissue factor structure region"
FT /note= "Tissue factor structure region"
FT 38..57 /label= Tissue_factor_signature
FT /label= Tissue_factor_signature
FT 40..226 /note= "Tissue factor structure region"
FT /note= "Tissue factor structure region"
FT 84..119 /label= Tissue_factor_domain
FT 235..255 /note= "Shows high homology to bacterial chemotaxis
FT /note= "Shows high homology to bacterial chemotaxis
FT sensory transducer signature"
XX
PN MO200123569-A1.
XX
XX 05-APR-2001.
XX

PF 29-SEP-2000; 2000MO-US026850.
XX
XX 29-SEP-1999; 99US-00408027.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Ballinger D, Ford J, Pace A, Sheridan J;
XX
XX WPI; 2001-266162/27.
DR N-PSDB; AAD03547.
XX
PT Polynucleotides encoding human cytokine receptor CG92, useful for
PT preventing, diagnosing and treating inflammation and disorders of blood
PT coagulation.
XX
PS Claim 10; Fig 1-3; 109pp; English.
XX
CC The present sequence is human cytokine receptor protein, designated as
CC CG92. CG92 is a member of the class II cytokine receptor (CRF2) family,
CC which includes R1 and R2 of chains of the IL-10 receptor complex, IFN-
CC alpha receptor complex, and tissue factor (TF). CG92 DNA and proteins are
CC used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate cytokine receptor expression such as inflammatory
CC disorders and disorders of blood coagulation. These disorders include
CC sepsis, thrombosis, acute pancreatitis, arthritis, vasculitis, lupus,
CC immune complex glomerulonephritis, diabetes, allograft and xenograft
CC transplantation, hepatitis, stroke and cancers. It is also used for
CC treating various immune deficiencies and disorders such as severe
CC combined immunodeficiency (SCID) and autoimmune disorders such as
CC multiple sclerosis, rheumatoid arthritis; nervous system disorders (e.g.,
CC Alzheimer's disease); sarcoidosis; leukaemia (e.g., erythroleukaemia);
CC inflammations such as graft versus host disease (GVHD), inflammatory
CC bowel disease and endotoxin shock; hyperproliferative disorders (e.g.,
CC psoriasis); cancers (e.g., non-Hodgkin's lymphoma, prostate cancer) and
CC bone degenerative diseases such as osteoporosis. CG92 cDNA is also used
CC in gene therapy. CG92 possesses cytokine and cell
CC proliferation/differentiation activity, immune regulating activity,
CC haematopoiesis regulating activity, tissue growth activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC activity. CG92 is also used in assays to identify modulators of cytokine
CC receptor expression and their activities
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 1080; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.8e-109; Mismatches 0; Gaps 0;
Matches 203; Conservative 0; Indels 0; Gaps 0;

QY 1 DEVAIIIPAPQNLSTLNKMKHLLMSPVIAFGETVYVSEYQGEYSLSYTHIMIPSSWC 60
DB 30 DEVAIIIPAPQNLSTLNKMKHLLMSPVIAFGETVYVSEYQGEYSLSYTHIMIPSSWC 89

QY 61 SLTEGPECDVTDDITATVPNNLRVRAVLGSGTSAMSLIKHPFRNNTILTRPCEMTTKDG 120
DB 90 SLTEGPECDVTDDITATVPNNLRVRAVLGSGTSAMSLIKHPFRNNTILTRPCEMTTKDG 149

QY 121 FHLVIELEDIGPQFEFLVAYMRREPAGAEHVKVNRSGGIPVHLETPMPPGAAYCVKQOTFV 180
DB 150 FHLVIELEDIGPQFEFLVAYMRREPAGAEHVKVNRSGGIPVHLETPMPPGAAYCVKQOTFV 209

QY 181 KAIGRYSAFSQTECEVQGEAIP 203
DB 210 KAIGRYSAFSQTECEVQGEAIP 232

RESULT 15
AAU04059
ID AAU04059 standard; protein; 311 AA.
XX
XX AAU04059;
XX
XX 23-OCT-2001 (first entry)
XX
XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2005, 02:33:14 ; Search time 23.4599 Seconds
(without alignments)
832.570 Million cell updates/sec

Title: US-09-745-792a-15

Perfect score: 1080

Sequence: 1 DEVAIIIPAPQNLSTNMK.....GRYSAPGQTECVQGAIP 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	16.0	337	2 I38500	interferon gamma r
2	162	15.0	349	2 JC6311	interferon recepto
3	159.5	14.8	325	2 A47003	cytokine receptor
4	158	14.6	332	2 A49947	interferon gamma r
5	151	14.0	560	2 S27387	interferon alpha r
6	142	13.1	590	2 A45283	interferon alpha/b
7	137.5	12.7	557	2 A32694	interferon alpha/b
8	122.5	11.3	578	2 I56215	interleukin-10 rec
9	117	10.8	292	1 KPRB3	tissue factor prec
10	115	10.6	295	1 KFHU3	tissue factor prec
11	112.5	10.4	575	2 A49667	interleukin-10 rec
12	103	9.5	292	1 KFBQ3	tissue factor prec
13	101.5	9.4	294	1 KEMS3	tissue factor prec
14	101.5	9.4	1118	1 A49724	protein-tyrosine-p
15	89.5	8.3	1427	2 I51669	tumor suppressor -
16	88	8.2	489	2 A31555	interferon gamma r
17	88	8.1	984	2 A39753	protein-tyrosine k
18	85.5	7.9	1557	2 D41214	protein-tyrosine-p
19	85.5	7.9	1630	2 C41214	protein-tyrosine-p
20	84	7.8	866	2 I56563	interleukin-3 rece
21	84	7.8	915	1 A55144	autocatalytic prote
22	83.5	7.7	329	2 T06873	quinolinate synthase
23	83.5	7.7	752	2 E72616	hypothetical prote
24	83	7.6	896	1 A35782	cytokine receptor
25	82.5	7.6	454	2 T20829	probable deoxyribo
26	82.5	7.6	681	2 S39058	hypothetical prote
27	82.5	7.6	716	2 H85089	integrin alpha 2 s
28	82.5	7.6	1170	2 I45914	VLA-2 protein homo
29	82.5	7.6	1178	2 S44142	

30	82	7.6	245	2 S53867	DNA (cytosine)-met
31	82	7.6	1258	2 JC5765	inositol polyphosp
32	81.5	7.5	1447	2 A54100	tumor suppressor p
33	81	7.5	2944	2 A54849	collagen alpha 1(V
34	80.5	7.5	227	2 T11483	cytochrome-c oxida
35	80.5	7.5	776	2 A82787	TonB-dependent rec
36	80.5	7.5	831	2 JQ1655	prolactin receptor
37	80.5	7.5	1181	2 A33998	integrin alpha-2 c
38	80.5	7.5	2051	2 T30938	receptor tyrosine
39	80	7.4	419	2 T10652	hypothetical prote
40	79.5	7.4	227	2 T11250	cytochrome-c oxida
41	79.5	7.4	227	2 T11053	cytochrome-c oxida
42	79	7.3	197	2 B96568	hypothetical prote
43	79	7.3	383	2 S67477	F420-nonreducing h
44	79	7.3	952	2 I50612	protein-tyrosine k
45	78.5	7.3	360	2 AF0247	probable exported

ALIGNMENTS

RESULT 1

I38500
interferon gamma receptor accessory factor-1 precursor - human

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004

C/Accession: I38500; I38501

R/Sch, J.J. Donnelly, R.J. Korenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S

Cell 76, 793-802, 1994

A/Title: Identification and sequence of an accessory factor required for activation of

A/Reference number: A49946; MUID:94170380; PMID:8124716

A/Accession: I38500

A/Molecule type: mRNA

A/Residues: 1-337 <RES>

A/Cross-references: UNIPROT:P38484; EMBL:U05875; NID:9463549; PIDN:AAA16955.1; PID:9463

A/Experimental source: clone pSKI

A/Accession: I38501

A/Molecule type: mRNA

A/Residues: 1-63, 'Q', '65-337 <RES>

A/Cross-references: EMBL:U05877; NID:9463551; PIDN:AAA16956.1; PID:9463552

A/Experimental source: clone pU3

C/Genetics:

A/Map position: 21

C/Keywords: cytokine receptor

Query Match 16.0%; Score 173; DB 2; Length 337;

Best Local Similarity 28.2%; Pred. No. 3e-08;

Matches 64; Conservative 31; Mismatches 96; Indels 36; Gaps 11;

Qy	1	DEVAIIIPAPQNLSTNMKGLMMSPVIAFGT--VYSVYQGEYESTYSHIWPSS 58
Db	25	DPLSQLPAPQHPKRLYNAGQVLSWEVYALNSNTRPVYVAVQKRTDYSKFTADIMSIGV 84
Qy	59	WCSLTGEGPCDVTDDITATVP-----YNLRVRAITGQTSAMSIL--KHPPNRNS 106
Db	85	NCTQITATGEC---DFTAASPAGFPMDVNTVRLRLRELGALHSAAWTMPMPQ--YRNV 138
Qy	107	TILTRPGMETTXGQFHLVIT-----ELIEDGQPGP--PLVAYMRREPAAEHYK--MVSNG 158
Db	139	TVGPPENIEVTPBEGSLIRFSSPFDIADTSTAFPCYVYVW--EKGGIQOVKQPFPSNS 196
Qy	159	IPVHLETMBPAGAYCVAAQTFFV---KAIRYSAPGQTECVQGAIP 201
Db	197	I--SLDNLKPSRYCYCQVQAOQLMKNNSNIRVGHLSNISCYETMADA 241

RESULT 2

JC6311
interferon receptor-class II cytokine receptor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: JC6311

R/Gibbs, V.C.; Pennica, D.

A:Cross-references: EMBL:106320; NID:g163187; P1DN:AAA02571.1; PID:g163188
A:Experimental source: Lung
A:Keywords: antiviral; cytokine receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

Query Match 14.0% Score 151; DB 2; Length 560;
Best Local Similarity 24.6%; Pred. No. 6.1e-06;
Matches 52; Conservative 38; Mismatches 87; Indels 34; Gaps 9;

Oy 6 LPAPQNLSTVSTNKKHLMLMSPVIAFGATVYVSEYQGESESLYTSI-----W--IP 56
Db 229 VSPSPENIQINADNOIYLUK-----DYPIENAFPOQWLAAPFKIIGNSDKKQIP 221
Oy 57 SSNCSLTEGBCDVTDDITATVPYNLRVATIGSOTSAMSLKHPENRSTILTRPGM-- 114
Db 282 N--CEVNTSTHCVPREVRSGIYVRASNGNGTSFWSBEKKEFTETKTIIFPPIVS 339
Oy 115 -ETTKGPHLVI---ELEDDGPQ---PEFLVATVWRKPGAEHRYQVRSGGIPVHLET 165
Db 340 KSTVDSLSHVSQSESESNNSVNOQLYPLIYEVIFWENTSNBRKYLEKRTNPI---FPD 396
Oy 166 MEGAAVCVCAQTFPKAIGRY--SAFSOTEC 194
Db 397 LKPLTYCVARALILENDRKNGSSFSPTVC 427

RESULT 6
A45283
Interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp
A:Reference number: A45283; MUID:92262522; PMID:1535935
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UB>
A:Cross-references: UNIPROT:P33896; GB:M89644; NID:g194111; P1DN:AAA37890.1; PID:g194112
A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIIP:102357)
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq
A:Reference number: I48423; MUID:95047447; PMID:7958966
A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 118-125 <RES>
A:Molecule type: DNA
A:Cross-references: EMBL:U06237; NID:g497103; P1DN:AAA65003.1; PID:g755810
A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 127-224 <R2>
A:Molecule type: DNA
A:Cross-references: EMBL:U06238; NID:g497104; P1DN:AA01749.1; PID:g755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <R3>
A:Cross-references: EMBL:U06239; NID:g497106; P1DN:AAA65004.1; PID:g510261
A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <R4>
A:Cross-references: EMBL:U06240; NID:g497108; P1DN:AAA65005.1; PID:g510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <R5>
A:Cross-references: EMBL:U06241; NID:g497110; P1DN:AAA65006.1; PID:g755812
A:Accession: I48428

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:U06242; NID:G497112; PID:AAA65007.1; PID:G755813
A:Accession: I48429
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:U06244; NID:G497114; PID:AAA65008.1; PID:G510265
C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

Query Match 13.1%; Score 142; DB 2; Length 590;
Best Local Similarity 24.9%; Pred. No. 4,4e-05;
Matches 49; Conservative 39; Mismatches 95; Indels 14; Gaps 8;

QY 6 LPAPONSVLSTNNKHLIAMSPTVIAPEGTYISVEYGEBSLYTSH--WIPSGCSLT 63
Db :
. 229 MPVGNTLVQDAGKSIVLKND-VIASADVLFRAQMLPGYSKSSGSDDKKPIPTCANV 287
QY 64 EGPGCDVTDDITATVPNVLRATLGQSOTASWSIKLPFRNRNSILRPGMEIR--XDF 121
Db :
288 QTHCVPSQDTVTYTGTFTFLVAQSEGNHTSWESEKTIDSKHILPPRPVITYTAMSDTL 347
QY 122 HLVIETLEDDL--GPQFEPLVAVWRREPDAEHHVMGVSCGIPVHLETMPGAAYCYAAQT 178
Db :
348 LVVYNQDSCTGDGLNYE--IIFF--ENTSNTKISMEDGP-EFTLNKLQLPITYCYGARV 402
QY 179 FVKAKIGRYSAFSGTEC 194
Db :
403 LFRALINKTSNFSEKLC 419

RESULT 7
A32694
Interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C:Accession: A32694; S17112
R:Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60; 225-224, 1990
A>Title: Genetic transfer of a functional human interferon alpha receptor into mouse ce
A:Reference number: A32694; MUID:90124633; PMID:2153461
A:Accession: A32694
A:Molecule type: mRNA
A:Residues: 1-557 <UZE>
A:Cross-references: UNIPROT:P17181; GB:J03171; NID:G184645; PID:AAA52730.1; PID:G30691
R:Lutfalla, G.
submitted to the EMBL Data Library, July 1991
A>Description: The structure of the human interferon alpha/beta receptor gene.
A:Reference number: S17112
A:Accession: S17112
A:Molecule type: DNA
A:Residues: 1-16 'A', 18-329, 'V', 343-557 <LUT>
A:Cross-references: EMBL:X60459; NID:G32671
C:Genetics:
A:Gene: GDB:IFNARI; IFNAR; IFRC
A:Cross-references: GDB:I20078; OMIM:107450
A:Map position: 21q22.1-21q22.1
A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C:Keywords: cytokine receptor; glycoprotein; status predicted <TR1>
P:1-21/Domains: transmembrane #status predicted <TR1>
P:437-455/Domains: transmembrane #status predicted <TR2>
P:50,58,81,88,110,172,254,313,314,376,416,453,507,518,537/Binding site: carbohydrate (A)

Query Match 12.7%; Score 137.5; DB 2; Length 557;
Best Local Similarity 22.1%; Pred. No. 0.00011;
Matches 50; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

6 LPAPONSVLSTNNKHLIAMSPTVIAPEGTYISVEYGEBSLYT-----SHIWPSWC 60

Db 229 LPPENIEVSQVONVYLKM-----DYTAAMTFQVQMLHFLKRNPNHLY---KWK 278
 QY 61 STGECPCDVTDTATVPYN-----LRYRATLGSQTSMS-----ILKH 100
 Db 279 QI---PDCENNVTTQCVFQNVFQKGYTLRLVQASDGNNTSWSSEIKFDTIQAFLLP 335
 QY 101 PPNRNSTLTTRPCMEITKDGFLVIT-----ELSDLGQFQEFVLVYMRREPQAEH 150
 Db 336 VFNIRS-----LSDSFHIYIGAPKQSGNTVDIDYPLIVE--IIFPENSNMAR 383
 QY 151 VGVWVGSGIPVHLEMTMEGAACVKAQ--TFPKAIGRASASQTEC 194
 Db 384 IIEKKT---DYVFNKLKPLVYCVARAHATWDEKLNKSSVPSDAVC 426

RESULT 8
 156215
 Interleukin-10 receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 156215
 R.Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
 J. Immunol. 152, 1821-1829, 1994
 A>Title: Expression cloning and characterization of a human IL-10 receptor.
 A:Reference number: 156215; MUID:94165477; PMID:8120391
 A:Accession: 156215
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-578 <RES>
 A:Cross-references: UNIPROT:Q13651; EMBL:U00672; NID:g482802; PIDN:AAA17896.1; PID:g4828
 C:Genetics:
 A:Gene: GDB:1110R; HL-10R
 A:Cross-references: GDB:330958; OMIM:146933
 A:Map position: 11q23.3-11q23.3
 C:Superfamily: interleukin-10 receptor IL10R
 C:Keywords: cytokine receptor

Query Match 11.3%; Score 122.5; DB 2; Length 578;
 Best Local Similarity 22.9%; Pred. No. 0.0027;
 Matches 51; Conservative 33; Mismatches 86; Indels 53; Gaps 8;
 QY 6 LPAPQNTSVLSTNMKHLIMSPVIAPEGTYYVSVEYGEYESLYTSHIWPSSWCSLTEG 65
 Db 26 LPSPSPWFEPFAEPFHILHTPIPNQSESTCYEAL-----LRGIESWMSISNCQSTLS 80
 QY 66 PECD-VTDDITATVPYNLRYRATLGSQTSMSILKHPNNNSTLT----- 110
 Db 81 YDLTAVTLDLHNSNGYRARVAVDGSRHSMWTNTNRFSDVTLTVGSVNLEIHNGFTL 140
 QY 111 -----RPGMEITKDGSHLVTELEDLQPF-EFLVAYMRREP-----AEHVKNV 154
 Db 141 GKTLQLPKPNAIPANDY-----ESIFSHREYEIAL-RKVPQNPFTTHKVKGHENFSLL 193
 QY 155 RSGGIPVHLEMTMEGAACVKAQTFVKAIGRASASQTECEV 197
 Db 194 TSGEVS-----GEFCVQVAPSVASRSNKMGMSKEBCISL 226

RESULT 9
 KFRB3
 tissue factor precursor - rabbit
 N:Alternate names: coagulation factor III
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: U00441; S23681
 R.Andrews, B.S.; Rehmetulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.
 Gene 98, 265-269, 1991
 A>Title: Conservation of tissue factor primary sequence among three mammalian species.
 A:Reference number: J00441; MUID:91200676; PMID:1840552
 A:Accession: J00441
 A:Molecule type: mRNA
 A:Residues: 1-292 <AMD>
 A:Cross-references: UNIPROT:P24055; GB:M55390; NID:g165696; PIDN:AAA63469.1; PID:g165697

A:Experimental source: brain
 R.Pasashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
 Thromb. Haemost. 66, 315-320, 1991
 A>Title: Molecule cloning, characterization and expression of cDNA for rabbit brain ti-
 A:Reference number: S23681; MUID:92081032; PMID:1746002
 A:Accession: S23681
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 33-292 <PAN>
 A:Cross-references: EMBL:X53521; NID:g1495; PIDN:CAA37597.1; PID:g3960170
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 C:Superfamily: tissue factor
 C:Keywords: blood coagulation; glycoprotein; lipoprotein; cholesterol bond; transmembrane
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-292/Product: tissue factor #status predicted <NAT>
 F:33-249/Domain: extracellular #status predicted <EXT>
 F:250-271/Domain: transmembrane #status predicted <TM>
 F:272-292/Domain: intracellular #status predicted <INT>
 F:41,114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:78-87,216-239/Disulfide bonds: #status predicted
 F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 10.8%; Score 117; DB 1; Length 292;
 Best Local Similarity 25.0%; Pred. No. 0.0036;
 Matches 57; Conservative 26; Mismatches 87; Indels 58; Gaps 11;
 QY 11 NTSVSTNMKHLIMSPVIAPEGTYYVSVEYGEYESLYTSHI-----WTPSSWCSLTE 64
 Db 41 NLTWSTYKFTLEWEP-----KSIDH-----YVTVQISTRLBNW--KSKCFLLTA 83
 QY 65 GPCPCDVTDTATV--PYNLRYRATLGSQTSMSILKHPNNNS-----TLTRGGM 114
 Db 84 ETBCDITBEVVDVQOTMARVLSIPRANGTGTGPEPSPRNSPEFTPYDNLGQFTI 143
 QY 115 E-ITDGFHLVTELD-----LGPQEPFLVAYMRREPQAEHVKNVRS 156
 Db 144 QSFQVGTGLNVTQDARTLVRRNGTFLSLRAVFGKDLNLTLYWR-----ASSGKKTAT 199
 QY 157 GGIPIHLEMTMEGAACVKAQTFVKAIGR--YSAFSQTECV-ENQGEA 201
 Db 200 TNTNEFLIDVDGSENYCFSVQAVIPSRKORSPESLTCRSBQGRA 247

RESULT 10
 KPFU3
 tissue factor precursor [validated] - human
 N:Alternate names: coagulation factor III
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: A43645; A47574; A28320; A29062; A29672; A29008
 R.Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
 Biochemistry 28, 1755-1762, 1989
 A>Title: Complete sequence of the human tissue factor gene, a highly regulated cellular
 A:Reference number: A43645; MUID:89247359; PMID:2719931
 A:Accession: A43645
 A:Molecule type: DNA
 A:Residues: 1-295 <MAC>
 A:Cross-references: UNIPROT:P13726; GB:J02846; NID:g339505; PIDN:AAA61152.1; PID:g33950
 R.Fisher, K.L.; Gorman, C.W.; Vohar, G.A.; O'Brien, D.P.; Lawn, R.M.
 Thromb. Res. 48, 89-99, 1987
 A>Title: Cloning and expression of human tissue factor cDNA.
 A:Reference number: A47574; MUID:88100453; PMID:3424286
 A:Accession: A47574
 A:Molecule type: mRNA
 A:Residues: 1-295 <RTS>
 A:Cross-references: GB:M27346; NID:g339507; PIDN:AAA63734.1; PID:g339508
 R.Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; L
 Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
 A>Title: Isolation of cDNA clones coding for human tissue factor: primary structure of
 A:Reference number: A94171; MUID:87260946; PMID:3037556
 A:Accession: A28320
 A:Molecule type: mRNA

A/Residues: 1-295 <SP1>
 A/Cross-references: GB:002931; NID:g339501; PIDN:AAA61150.1; PID:g339502
 R/Moritssey, J.H.; Fakhrat, H.; Edgington, T.S.
 Cell 50, 129-135, 1987
 A/Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the
 A/Reference number: A29062; MUID:87244317; PMID:3297348
 A/Accession: A29062
 A/Molecule type: mRNA
 A/Residues: 1-295 <MOR>
 A/Cross-references: GB:002931; NID:g339501; PIDN:AAA61150.1; PID:g339502
 A/Note: part of this sequence, including the amino end of the mature protein, was confir
 R/Schmidt, E.M.; Wen, D.; Broca Jr., G.T.; Milech, J.P.; Flandermeier, R.R.; Siegel,
 Biochemistry 26, 5234-5238, 1987
 A/Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.
 A/Reference number: A29672; MUID:88050796; PMID:2823875
 A/Accession: A29672
 A/Molecule type: mRNA
 A/Residues: 1-259, 'A', 261-295 <SCA>
 A/Cross-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
 R/Bach, R.; Konigsberg, W.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A/Title: Human tissue factor contains thioester-linked palmitate and stearate on the cy
 A/Reference number: A37422; MUID:89000604; PMID:3166978
 A/Content: annotation; disulfide bonds and fatty acid binding site
 A/Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C/Comment: Expression of tissue factor can be induced in a variety of tissues by certai
 C/Genetics:
 A/Gene: GDB:F3
 A/Cross-references: GDB:119895; OMIM:134390
 A/Map position: 1p22-1p21
 A/Intons: 34/1; 71/2; 138/1; 197/3; 251/1
 C/Superfamily: tissue factor
 A/Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
 F:1-32/Domain: signal sequence; #status predicted <SIG>
 F:33-295/Product: tissue factor #status experimental <MAT>
 F:33-251/Domain: extracellular #status predicted <EXT>
 F:252-274/Domain: transmembrane #status predicted <TM>
 F:215-295/Domain: intracellular #status predicted <INT>
 F:43/Binding site: carbohydrate bonds: #status experimental
 F:81-89, 218-241/Disulfide bonds: #status experimental
 F:156,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:277/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 10.6%; Score 115; DB 1; Length 295;
 Best Local Similarity 24.1%; Pred. No. 0.0056;
 Matches 56; Conservative 29; Mismatches 95; Indels 46; Gaps 11;

QY 8 APONLSVSTNMKHLMSPIVAPGETVYVSVEYQGEYSLYTSHIWPSSWCSLTGPE 67
 DB 40 AAYVLTWKSSTNFKTILEMEP--KEVNOV-YTVQISTK-----SGDW--KSKCFYTTDT 88
 QY 68 CDVTDDITATY--PYNLRVATLGSGTSAMSLKHPNRS-----TLTRPGME-I 116
 DB 89 CDLTDEIVKDVQKQYTLARVPSYPAGNVESTGACEPLYENSPFTPYLETNLGQPTIQSF 148
 QY 117 TKDGFHLVLELD-----LGPFELVAVYWRPEAEHVKVRSGLI 159
 DB 149 EYGTGKLVVYEDRTLVRRNNTFLSLRDVFGKOLITLVYKSSSSGKTKAKT-----NT 204
 QY 160 PVHLETMEPGAAYCVKAQTFV--KAIGRYSAFSQTECV-EVQGE 200
 DB 205 NEFLIDVDKGBNVCFSYQAVIPSRVNRKSTDSFEGCQGEKGE 248

RESULT 11
 A49667
 Interleukin-10 receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: A49667
 R/Ho, A.S.; Liu, Y.; Khan, T.A.; Han, D.H.; Bazan, J.F.; Moore, K.W.
 Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
 A/Title: A receptor for interleukin 10 is related to interferon receptors.

A/Reference number: A49667; MUID:94068585; PMID:8248239
 A/Accession: A49667
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-575 <RSS>
 A/Cross-references: UNIPROT:Q61727; GB:L12120; NID:g437615; PIDN:AAA6156.1; PID:g43761
 C/Genetics:
 A/Gene: IL10R
 C/Superfamily: interleukin-10 receptor IL10R
 C/Keywords: cytokine receptor

Query Match 10.4%; Score 112.5; DB 2; Length 575;
 Best Local Similarity 28.4%; Pred. No. 0.022;
 Matches 31; Conservative 15; Mismatches 54; Indels 9; Gaps 2;

QY 6 LPAPONSVSTNMKHLMSPIVAPGETVYVSVEYQGEYSLYTSHIWPSSWCSLTG 65
 DB 26 LPSPSYWFPARRPFGHLLHKPILPNOSSESYTEVALEK-----QYGNSTWMDIHICRAQA 80
 DB 81 LSCDLTFTLDVHRSYGVARAVRVDNSQYSWMTTETRTFVDEVILT 129

RESULT 12
 KFB03
 tissue factor precursor - bovine
 N/Alternate names: coagulation factor III
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: JQ1319
 R/Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
 Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
 A/Title: cDNA and amino acid sequences of bovine tissue factor.
 A/Reference number: JQ1319; MUID:92109720; PMID:1764085
 A/Accession: JQ1319
 A/Molecule type: mRNA
 A/Residues: 1-292 <TRK>
 A/Cross-references: UNIPROT:P30931; GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g24143
 A/Experimental source: adrenal gland
 A/Note: part of this sequence, including the amino end of the mature protein, was confir
 C/Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C/Comment: Expression of tissue factor can be induced in a variety of tissues by certai
 C/Superfamily: tissue factor
 A/Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembran
 F:1-35/Domain: signal sequence; #status predicted <SIG>
 F:36-292/Product: tissue factor #status experimental <MAT>
 F:36-248/Domain: extracellular #status predicted <EXT>
 F:249-271/Domain: transmembrane #status predicted <TM>
 F:272-292/Domain: intracellular #status predicted <INT>
 F:43,153,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:81-89, 215-238/Disulfide bonds: #status predicted
 F:118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 9.5%; Score 103; DB 1; Length 292;
 Best Local Similarity 20.3%; Pred. No. 0.07;
 Matches 44; Conservative 31; Mismatches 88; Indels 54; Gaps 8;

QY 11 NLSVLTNMKHLMSPIVAPGETVYVSVEYQGEYSLYTSHI-----NIPSSWCSLTG 64
 DB 43 NITWKSSTNFKTILEMEP-----KPINHVYVQISPRLGNN--KSKCFYTT 85
 QY 65 GPEDVTDDITATYVPYNLRVATLGSGTSAMSLKHPNRS-----STLTRPGME-I 116
 DB 86 NTECDVTDEIVKDVQKQYTLARVLSYPADTSSVTPPEPTNSPFTPYLETNLGQPTIQSF 145
 QY 117 TKDGFHLVLELD-----LGPFELVAVYWRPEAEHVKVRSGLI 159
 DB 146 EYGTGKLVVYQDARTLVRRNSAFLSLRDVFGKOLNTLVYKSSSGKATNTNG-- 203
 QY 160 PVHLETMEPGAAYCVKAQTFV--KAIGRYSAFSQTEC 194

Db 204 --FLAIDVDKGENYCFHQAIVLLSRVYNQKSPESPIC 238

RESULT 13

KFMS3

tissue factor precursor - mouse
N/Alternate names: coagulation factor III

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: A33318; A39046

R/Hartzell, S.; Ryder, K.; Ianahan, A.; Lau, L.F.; Nathans, D.

Mol. Cell. Biol. 9, 2567-2573, 1989

A/Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein hc

A/Reference number: A33318; MUID:89343974; PMID:2761539

A/Accession: A33318

A/Molecule type: mRNA

A/Residues: 1-294 <HAR>

A/Cross-references: UNIPROT: P20352; GB:M26071; NID:G201924; PIDN:AAA40414.1; PID:G201925

R/Ranganathan, G.; Blattl, S.P.; Sudramaniam, M.; Fass, D.N.; Mathle, N.J.; Getz, M.J.

J. Biol. Chem. 266, 496-501, 1991

A/Title: Cloning of murine tissue factor and regulation of gene expression by transformi

A/Reference number: A39046; MUID:91093171; PMID:1985911

A/Accession: A39046

A/Molecule type: mRNA

A/Residues: 1-25, '1', '27-294 <RAN>

A/Cross-references: GB:M57896; GB:U05713; NID:G201926; PIDN:AAA63400.1; PID:G201927

A/Note: 26-Thr was also found

C/Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor

C/Summary: Expression of tissue factor can be induced in a variety of tissues by certain

C/Keywords: blood coagulation; glycoprotein; lipoprotein; cholesterol bond; transmembrane

F.1-29/Domain: signal sequence #status predicted <SIG>

F.30-294/Product: tissue factor #status predicted <EXT>

F.30-251/Domain: extracellular #status predicted <EXT>

F.25-274/Domain: transmembrane #status predicted <TM>

F.37-57, 169, 200/Binding site: carbohydrate (asn) (covalent) #status predicted

F.75-83, 218-241/Disulfide bond: #status predicted

F.275/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 9.4%; Score 101.5; DB 1; Length 294;

Best Local Similarity 23.7%; Pred. No. 0.097;

Matches 54; Conservative 31; Mismatches 80; Indels 63; Gaps 13;

Db 11 NLSTLSTMMKHLMMSPVIAAGETVY-YSEVYQGEYSLSYSHIMSSCSLTEGPEC 69

Db 37 NLWISIDTDFKTLISWQ---PKPTNYTYTVOISDR-----SRNW--KNKCFSTTDECC 84

QY 70 VTDDIT--ATVPYMLRYRATL-----GSO-----TSMSILHHPNRNSTLL 109

Db 85 LTDEIVDVMTWAYAKVLSPRRNSVHGDDQLVHGEPPFTNAPKFLPY---RDYNL 140

QY 110 TRPGM-BITKDGPHLVLEL-----LQDFEFLVAVR-REPGAEEH 150

Db 141 GQPIVIOQFEDQGRKLVVVXDSLTVLRKNGTFLTLRQVFKDGYIITYKKGSTCKTN 200

QY 151 VKWVRSGGIPVHLETPBGAAYC--VKAQTFVVAIGRYSAFSCTECE 196

Db 201 ITNINERSIV---EEGVSYCFVQAMTFSRKTONSPGSSITVCTE 243

RESULT 14

A49724

protein-tyrosine-phosphatase (BC 3.1.3.48), receptor type H precursor - human

N/Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SAP-1

C/Species: Homo sapiens (man)

C/Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C/Accession: A49724

R/Matocak, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K.

J. Biol. Chem. 269, 2075-2081, 1994

A/Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase an

A/Reference number: A49724; MUID:94124561; PMID:8294459

A/Accession: A49724

A/Molecule type: mRNA

A/Residues: 1-1118 <HATO>

A/Cross-references: UNIPROT: Q15426; GB:D15049; NID:G475003; PIDN:BA03645.1; PID:G475004

C/Genetics:

A/Gene: GDB:PTPRH; SAP-1

A/Cross-references: GDB:305504

A/Map position: 19q13.4-19q13.4

A/Note: highly expressed in colon and pancreatic cancer cells but not in the normal cel

C/Summary: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repe

C/Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric monoe

F.1-27/Domain: signal sequence #status predicted <SIG>

F.28-110/Product: protein-tyrosine-phosphatase, receptor type H #status predicted <MAT>

F.28-761/Domain: extracellular #status predicted <EXT>

F.116-199/Domain: fibronectin type III repeat homology <3FNB>

F.205-289/Domain: fibronectin type III repeat homology <3FNC>

F.296-379/Domain: fibronectin type III repeat homology <3FND>

F.385-468/Domain: fibronectin type III repeat homology <3FNE>

F.474-558/Domain: fibronectin type III repeat homology <3FNF>

F.564-658/Domain: fibronectin type III repeat homology <3FNG>

F.667-737/Domain: fibronectin type III repeat homology <3FNH>

F.762-778/Domain: transmembrane #status predicted <TM>

F.779-1118/Domain: intracellular #status predicted <INT>

F.846-1070/Domain: protein-tyrosine-phosphatase homology <PTP1>

F.35, 78, 83, 107, 132, 149, 172, 196, 203, 286, 304, 312, 329, 352, 376, 383, 401, 436, 439, 470, 490, 558, 5

F.1022/Active site: Cys (phosphocysteine intermediate) #status predicted

F.1028/Binding site: substrate phosphate (Arg) #status predicted

Query Match 9.4%; Score 101.5; DB 1; Length 1118;

Best Local Similarity 24.3%; Pred. No. 0.53;

Matches 49; Conservative 18; Mismatches 76; Indels 59; Gaps 8;

QY 47 SLTSHIWRPSSWCSLTSBECVDYDDITATVP---YVLRVATIGSOTS-AMSLIKHP 102

Db 93 SLTGSVWWEK-----DVNNSVGTVTATAPNVRNLRKRAQNTSSIALTWEVDPGD 146

QY 103 NENSTTLTRPGMEITKDG-----FLVLELDLGPQFELVAVY-----R 142

Db 147 PONSRY---GVEYTGDDGAGTRTATNTITVDSLEGCLYARSMWVGKNGINSRRT 202

QY 143 REPGAEEHVKVVRSGI-----PVHLETPBGAAYCYKAQTF----- 179

Db 203 NATYAHNPVRKPSGSDHQLHPGLGPRMHRPTELDLRTSLAEWVAEQRLTEQTP 262

QY 180 --VKAIGRYSAFSQTECEVQ 199

Db 263 SPVDLGLGSLTSGVWWEKDG 284

RESULT 15

151669

tumor suppressor - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: 151669

R/Pierceli, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R.

Dev. Biol. 166, 654-665, 1994

A/Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the

A/Reference number: 151668; MUID:95113183; PMID:7813784

A/Accession: 151669

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1427 <PIE>

A/Cross-references: UNIPROT: Q91562; EMBL: U10986; NID:G606873; PIDN:AAA70168.1; PID:G6068

C/Genetics:

A/Gene: XDCCA

Query Match 8.3%; Score 89.5; DB 2; Length 1427;

Best Local Similarity 21.0%; Pred. No. 9.2;

Matches 48; Conservative 26; Mismatches 74; Indels 81; Gaps 9;

QY 9 PONSIVSLTMKHL-LMMSVIAAGETVYVSEY-----QGEYSLSYSHIMY--- 55

Db 626 PONSIVSLTMKHL-LMMSVIAAGETVYVSEY-----QGEYSLSYSHIMY--- 55

626 PONSIVSLTMKHL-LMMSVIAAGETVYVSEY-----QGEYSLSYSHIMY--- 55

626 PONSIVSLTMKHL-LMMSVIAAGETVYVSEY-----QGEYSLSYSHIMY--- 55

626 PONSIVSLTMKHL-LMMSVIAAGETVYVSEY-----QGEYSLSYSHIMY--- 55

626 PONSIVSLTMKHL-LMMSVIAAGETVYVSEY-----QGEYSLSYSHIMY--- 55

626 PONSIVSLTMKHL-LMMSVIAAGETVYVSEY-----QGEYSLSYSHIMY--- 55

Qy 56 -----PSSWCSLTGPECCDVTDDITATVPYNLRVPAITLGSQTS 94
 Db 685 GLEKGSQYSPQVAMTVNGTGPSSSDWYTAETPENDLDSCQVDPQPSLHVPLTTSTIMS 744
 Qy 95 WSLIKHPFNNSITLTTRPGMEITKDGFHLVIELEDLGPQPEFLVAYWRREPGAEHVMV 154
 Db 745 WT--PPLNPN--IVR-----GYITGVGVSPYAE--TVRV 774
 Qy 155 RSGGIPVHLEMTBEPGAAYCVAAQTFFVKAIGRYSAFSQTECVVOGEAIP 203
 Db 775 DSKQRYYSIENLEBSSHVYISLKAFFNA-----GEGVP 807

Search completed: February 25, 2005, 02:45:39
 Job time : 25.4539 sec8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 25, 2005, 02:24:39 ; Search time 107.724 Seconds
(without alignments)
964.985 Million cell updates/sec

Title: US-09-745-792A-15

Perfect score: 1080

Sequence: 1 DEVALIPAPQNTSLVSTNMK.....GRYSAPQRECEVQGEAIP 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot_03:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1080	100.0	311	1	120S HUMAN
2	712	65.9	147	1	Q81Y55
3	173	16.0	337	1	INGS HUMAN
4	173	16.0	442	2	Q9PVJ9
5	173	16.0	569	2	Q9YH00
6	164.5	15.2	231	2	Q96A41
7	160	14.8	349	1	110S MOUSE
8	160	14.8	351	1	Q8VHM7
9	159.5	14.8	325	1	110S HUMAN
10	159.5	14.8	325	2	Q9BUT4
11	159.5	14.8	327	2	Q6ZVU9
12	158	14.6	332	2	Q63953
13	158	14.6	332	2	Q78EC1
14	151.5	14.0	262	2	Q6UWM1
15	151.5	14.0	263	2	Q969J5
16	151	14.0	560	1	INRI BOVIN
17	150	13.9	435	1	Q7ZT26
18	149	13.8	213	2	Q8C352
19	147.5	13.7	553	1	120R HUMAN
20	146	13.5	546	1	120R MOUSE
21	146	13.5	569	2	Q99ND6
22	144	13.3	301	2	Q7ZT35
23	142	13.1	560	1	INRI SHEEP
24	142	13.1	580	1	INRI MOUSE
25	139	12.9	505	1	Q6DCU5
26	138	12.8	530	2	Q80UR8
27	137.5	12.7	203	2	Q7ZT05
28	137.5	12.7	557	1	INRI HUMAN
29	137.5	12.7	557	2	Q8WTZ2
30	136	12.6	362	2	Q764M7
31	136	12.6	508	2	Q9YHV9

32	136	12.6	590	2	Q80UJ3	Q80UJ3	mus musculus
33	135	12.5	508	2	Q6QIU4	Q6QIU4	gallus galli
34	135	12.5	508	2	Q9PVX0	Q9PVX0	gallus galli
35	130.5	12.1	244	2	Q8IV66	Q8IV66	homo sapien
36	128	11.9	341	2	Q9YGC8	Q9YGC8	gallus galli
37	128	11.9	560	2	Q764M8	Q764M8	mus musculus
38	126.5	11.7	491	2	Q8IZ18	Q8IZ18	homo sapien
39	126.5	11.7	520	2	Q8IU57	Q8IU57	homo sapien
40	126.5	11.7	521	2	Q6ZML8	Q6ZML8	homo sapien
41	125.5	11.6	338	2	Q80UG2	Q80UG2	tetradon n
42	123	11.4	209	2	Q96SH7	Q96SH7	homo sapien
43	122.5	11.3	333	2	Q7ZT30	Q7ZT30	tetradon n
44	122.5	11.3	578	1	110R HUMAN	Q13651	homo sapien
45	119.5	11.1	336	2	Q80UE8	Q80UE8	tetradon n

ALIGNMENTS

RESULT 1
ID 120S HUMAN STANDARD; PRT; 311 AA.
AC Q6UX10: 06P438; Q8YAJ7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Interleukin-20 receptor beta chain precursor (IL-20R-beta) (IL-20R2) (UNQ557, P01114).
GN Name=IL20RB; Synonyms=DIRS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.V., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Hendel S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RT Genome Res. 13:2265-2270(2003).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Cervix; and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,
RA Diatchenko L., Marisana K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boufield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gough J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywicki M.I., Skaleka U., Smilley D.E.,
RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]
 RP SEQUENCE OF 30-44 (ISOFORM 1).
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 [4]
 RN SUBUNIT, LIGAND BINDING, AND TISSUE SPECIFICITY.
 RX MEDLINE=21097717; PubMed=1116236; DOI=10.1016/S0092-8674(01)00187-8;
 RA Blumberg H., Conklin D., Xu W.F., Grosseman A., Brender T.,
 RA Carroll S., Bagan W., Foster D., Haldeman B.A., Hammond A., Haugen H.,
 RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parish-Novak J.,
 RA Prunkard D., Sexson S., Sprecher C., West J.,
 RA Whitmore T.E., Yao L., Knechle M.K., Dale B.A., Chandrasekhar Y.A.;
 RT "Interleukin 20: discovery, receptor identification, and role in
 epidermal function.";
 RL Cell 104:9-19(2001).
 [5]
 RN SUBUNIT, AND LIGAND BINDING.
 RX PubMed=11564763;
 RA Dumoutier L., Leemans C., Lejeune D., Kotenko S.V., Renauld J.-C.;
 RT "STAT activation by IL-19, IL-20 and mda-7 through IL-20 receptor
 complexes of two types.";
 RL J. Immunol. 167:3545-3549(2001).
 [6]
 RN SUBUNIT, AND LIGAND BINDING.
 RX PubMed=12351624; DOI=10.1074/jbc.M205114200;
 RA Parrish-Novak J., Xu W., Brender T., Yao L., Jones C., West J.,
 RA Brandt C., Jelinek L., Madden K., McKernan P.A., Foster D.C.,
 RA Jagers S., Chandrasekhar Y.A.;
 RT "Interleukins 19, 20, and 24 signal through two distinct receptor
 complexes: Differences in receptor-ligand interactions mediate unique
 biological functions.";
 RL J. Biol. Chem. 277:47517-47523(2002).
 [7]
 RN SUBUNIT, AND LIGAND BINDING.
 RX PubMed=1580208; DOI=10.1021/bi0354583;
 RA Pletnev S., Magracheva E., Kozlov S., Tobin G., Kotenko S.V.,
 RA Wlodawer A., Zdanov A.;
 RT "Characterization of the recombinant extracellular domains of human
 Interleukin-20 receptors and their complexes with interleukin-19 and
 Interleukin-20.";
 RL Biochemistry 42:12617-12624(2003).
 CC -1- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and
 CC IL24. The IL22RA1/IL20RB dimer is a receptor for IL20 and IL24.
 CC -1- SUBUNIT: Heterodimer with IL20RA and heterodimer with IL22RA1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q6UXL0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q6UXL0-2; Sequence=VSP 011499, VSP 011500;
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in skin
 CC and testis. Highly expressed in psoriatic skin.
 CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL: AY3589305; AA086672.1; -;
 DR EMBL: BC027449; AA827449.1; -;
 DR EMBL: BC063696; AA63696.1; -;
 DR Genew; HGNC:6004; IL20RB.
 DR MIM: 605621; -;
 DR InterPro; IPR000282; Cytok_receptor_2.

DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR Pfam; PF0041; FN3_1.
 DR PROSITE; PS00853; FN3_1.
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 39
 FT CHAIN 30 311 Interleukin-20 receptor beta chain.
 FT DOMAIN 30 233 Extracellular (potential).
 FT TRANSMEM 234 254 Potential.
 FT DOMAIN 255 311 Cytoplasmic (potential).
 FT DOMAIN 36 137 Fibronectin type-III 1.
 FT DOMAIN 144 228 Fibronectin type-III 2.
 FT DISUPTID 202 223 By similarity.
 FT CARBOHYD 40 40 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 134 134 N-linked (GlcNAc...) (potential).
 FT VARSPPLIC 1 47 Missing (in isoform 2 and isoform 3).
 FT VARSPPLIC 48 142 Missing (in isoform 2).
 FT VARSPPLIC 142 1500 /FTID-VSP 011499.
 SQ SEQUENCE 311 AA; 35076 MW; FP366DS18116D9E3 CRC64;
 Query Match 100.0%; Score 1080; DB 1; Length 311;
 Best Local Similarity 100.0%; Pred. No. 8.3e-94;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVATLPAPQNVSTWTKHLMSPVAPAGETVYVVEGVEESLTSITWIPSSMC 60
 DB 30 DEVATLPAPQNVSTWTKHLMSPVAPAGETVYVVEGVEESLTSITWIPSSMC 89
 QY 61 SLTEGPECDVTDITATVPYNLRATVIGSOTSAMSLKHPNRSITLIRPGMEITDGG 120
 DB 90 SLTEGPECDVTDITATVPYNLRATVIGSOTSAMSLKHPNRSITLIRPGMEITDGG 149
 QY 121 FHLVLEEDLPQPEFPLVAYWRREPAGAEHVYVMSGGIPVHLETWEPGAAYCVAKQTFV 180
 DB 150 FHLVLEEDLPQPEFPLVAYWRREPAGAEHVYVMSGGIPVHLETWEPGAAYCVAKQTFV 209
 QY 181 KAIGRYSAFSQTECVGGEALP 203
 DB 210 KAIGRYSAFSQTECVGGEALP 232
 RESULT 2
 ID 081YV5 PRELIMINARY; PRT; 147 AA.
 AC 081YV5;
 DT 01-MAR-2003 (TRMBLrel. 23, Created)
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
 DE MGC34923 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins L.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnski M.I., Skalka U., Small D.E., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC033292; AA033282.1;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR008957; FN_III-like.
 SO SEQUENCE 147 AA; 16945 MW; 71BAF49274618999 CRC64;
 Query Match 65.9%; Score 712; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 2,3e-59;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 MKHLWMSPIVAGETVYVSEVQGEYSLYTSHWIPSGMCSLTGEGPCDVTDDITATV 78
 DB 1 MKHLWMSPIVAGEVTVYVSEVQGEYSLYTSHWIPSGMCSLTGEGPCDVTDDITATV 60
 QY 79 PYNLRVATVGSQTSAMSLKHPNRSITLTPRGMEITKDFGLVLEEDLGPQEPFLV 138
 DB 61 PYNLRVATVGSQTSAMSLKHPNRSITLTPRGMEITKDFGLVLEEDLGPQEPFLV 120
 QY 139 AYWRREPQAE 149
 DB 121 AYWRREPQAE 131
 RESULT 3
 INGS_HUMAN STANDARD; PRT; 337 AA.
 AC P38484; Q9BTL5;
 ID 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon-gamma receptor beta chain precursor (Interferon-gamma
 DE receptor accessory factor-1) (AF-1) (Interferon-gamma transducer-1).
 GN Name=IFNGR2; Synonyms=IFNGT1;
 OS Homo sapiens (Human).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=lung fibroblast;
 RX MEDLINE=94110380; PubMed=8124716; DOI=10.1016/0092-8674(94)90354-9;
 RA Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N.,
 RA Emanuel S.L., Schwartz B., Miki T., Pestka S.;
 RT "Identification and sequence of an accessory factor required for
 RT activation of the human interferon gamma receptor";
 RL Cell 76:793-802(1994).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Pelinold E.A., Grouse L.H., Dere J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile P.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange S.J.,
 RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahney J., Helton B., Ketterman M., Wadan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywnski M.I., Skalka U., Small D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP SEQUENCE OF 1-24 FROM N.A.
 RX MEDLINE=97067142; PubMed=8910544; DOI=10.1074/jbc.271.46.28947;
 RA Rhee S., Ebensperger C., Dembic Z., Pestka S.;
 RT "The structure of the gene for the second chain of the human
 RT interferon gamma receptor";
 RL J. Biol. Chem. 271:28947-28952(1996).
 CC -1- FUNCTION: Part of the receptor for interferon gamma. Required for
 CC signal transduction. This accessory factor is an integral part of
 CC the IFN-gamma signal transduction pathway and is likely to
 CC interact with GAF, JAK1, and/or JAK2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 DR EMBL: U05875; AAA16955.1; -;
 DR EMBL: U05877; AAA16956.1; -;
 DR EMBL: BC003624; AA003624.1; -;
 DR EMBL: U06755; AAC52066.1; -;
 DR PIR: I38500; I38500.
 DR Genew: HGNC:5440; IFNGR2.
 DR H-InvDB: HIX0016076; -;
 DR MIM: 147569; -;
 DR MIM: 209950; -;
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 DR GO: GO:0004906; F:interferon-gamma receptor activity; TAS.
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 DR GO: GO:0009618; P:response to pathogenic bacteria; TAS.
 DR GO: GO:000615; P:response to virus; TAS.
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam: PF00041; fn3; 1.
 DR PROSITE: PS50853; FN3; 2.
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 27
 FT CHAIN 28 337
 FT DOMAIN 28 247
 FT TRANSMEM 248 268
 FT DOMAIN 269 337
 FT DOMAIN 31 129
 FT DOMAIN 139 229
 FT CARBOHYD 56 56
 FT CARBOHYD 85 85
 FT CARBOHYD 110 110
 FT CARBOHYD 137 137
 FT CARBOHYD 219 219
 FT CARBOHYD 231 231
 FT VARIANT 64 64
 FT R -> Q.
 SO SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64;
 Query Match 16.0%; Score 173; DB 1; Length 337;
 Best Local Similarity 28.2%; Pred. No. 6.7e-08;
 Matches 64; Conservative 31; Mismatches 96; Indels 36; Gaps 11;

QY DEVALIPAPONISVLSTNMKHLMSRPVLAPEGT---VYYSVYQGEYELVLSHMISS 58
 Db DPISQAPAPHPKPKRLVYNQGVLSMEPVALSINSTRVYVRVQFKTDSKMFADIMSIGV 84
 QY WCSLTGPECDVDYDITATVP-----YNLRVATGSGOTSAMSLP---KHPFNNS 100
 Db NCQGITATEC-----DTPAASPSAGFPMDFNVTYLRRLAEIGALHSAMVTPMQH---YANV 133
 QY TILTRPCEMITKDFHVLV-----ELEDIGPGE-FLVAVYVRREPGAEHHYK-MVNSGC 156
 Db TVGPPENIEVTPGEGSLITRFSSPDPIADTSTAFCYVYHYW--EKGGIQQKGFRRNS 196
 QY IPHLELMEBGAAYCYKQATFV---KALGRSAPSQTECVYQGEA 201
 Db 197 I--SLDLKESRYVCLQVOQAQLMKNKSNLFRVGHLSNLSICYTMDA 241

RESULT 4				
ID	Q9PVJ9	PRELIMINARY;	PRT;	442 AA.
AC	Q9PVJ9;			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Interferon alpha/beta receptor 1 (Fragment).			
GN	Name=IFNARI;			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99177346; PubMed=10077530;			
RA	Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;			
RT	"Comparative genomic analysis of the interferon/interleukin-10			
RT	receptor gene cluster.";			
RL	Genome Res. 9:242-250(1999).			
DR	EMBL; AF082667; AAD13679.1; -.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0004896; F:hematopoietin/interferon-claas (D200-domain. . .; IEA.			
DR	InterPro; IPR000282; F:receptor activity; IEA.			
DR	InterPro; IPR003961; FN_III.			
DR	InterPro; IPR008957; FN_III-like.			
DR	SMART: SM00060; FN3; 2..FN_III-like.			
DR	PROSITE; PSS0853; FN3; 1.			
KW	Receptor.			
FT	NON TRR			
FT	442	442		
SQ	SEQUENCE	442 AA;	49877 MW;	839EBE92170609E0 CRC64;
Query Match 16.0%; Score 173; DB 2; Length 442;				
Best Local Similarity 27.0%; Pred. No. 9.3e-08;				
Matches 60; Conservative 27; Mismatches 91; Indels 44; Gaps 8;				

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09YHWO
ID 09YHWO PRELIMINARY: PRT: 569 AA.
AC 09YHWO:
DT 01-MAY-1999 (TREMBLrel). 10, Created
DT 01-MAY-1999 (TREMBLrel). 10, Last sequence update)
DE 01-MAY-2004 (TREMBLrel). 26, Last annotation update)
DR Interferon alpha/beta receptor 1.
GN Name=IFNARI;
OS Gallus gallus (Chicken).
OC Archaeoptila; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9177346; Pubmed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster";
RL Genome Res. 9:242-250(1999).
DR EMBL; AF082664; AADI3659.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; CytoK_receptor_2.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR SMART; SM00060; FN3_2.
DR PROSITE; PSS0883; FN3; 1.
DR SEQUENCE 569 AA; 64055 MW; 6A757DDFB891E605 CRC64;
Q0

```

RESULT 5

RESULT 6	
096A41	
ID	096A41
AC	096A41;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, last annotation update)
DE	Soluble cytokine class II receptor, short isoform precursor
DE	(Interleukin 22-binding protein CRP2-10) (Class II cytokine receptor
DE	(IL22RA2).
GN	Name=CRP-S1; Synonyms=IL-22BP, IL22BP, IL22RA2; ORFNames=UNQ5793;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxId=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Mammary gland;
XC	MDLLINE=21518574; PubMed=11607789; DOI=10.1038/sj.gene.6363786;

RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toechi L., Kunz S.,
 RA Moik K., Asadullah K., Sabat R.;
 RT "A novel, soluble homologue of the human IL-10 receptor with
 RT preferential expression in placenta."; [Gene Immun. 2:329-334\(2001\)](#).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RA Dumoutier L., Lejeune D., Renaud J.C.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21286453; PubMed=11390454;
 RA Kotenko S.V., Iotova L.S., Mironchukchenko O.V., Esterova E.,
 RA Dickensheets H., Donnelly R.P., Pestka S.;
 RT "Identification, cloning, and characterization of a novel soluble
 RT receptor that binds IL-22 and neutralizes its activity."; [J Immunol. 166:7096-7103\(2001\)](#).
 RL [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21396522; PubMed=11481447; DOI=10.1101/gr.1293003;
 RA Xu W., Pressnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,
 RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutemeyer S.,
 RA Yao L., Whitmore T.E., Chandrasekhar Y., Grant P.J., Maurer M.,
 RA Ullrich L., Storey H., Brander T., Hammond A., Topouzis S.,
 RA Clegg C.H., Foster D.C.;
 RT "A soluble class II cytokine receptor, IL-22RA2, is a naturally
 RT occurring IL-22 antagonist."; [Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516\(2001\)](#).
 RL [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
 RA Eaton D., Foster J., Gimaldi C., Gu Q., Hase P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robble B., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagstad A.,
 RA Vanden R., Watanabe C., Wileand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment."; [Genome Res. 13:2265-2270\(2003\)](#).
 RL EMBL; AJ131161; CAC85634.1; -;
 DR EMBL; AJ297262; CAC83097.1; -;
 DR EMBL; AY040566; AAK85714.1; -;
 DR EMBL; AY044429; AAK91775.1; -;
 DR EMBL; AY358111; AAC8478.1; -;
 DR HSSP; P24055; 1A21.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR Interpro; IPR000282; Cytok_receptor_2.
 DR Interpro; IPR008957; FN_III-like.
 DR Receptor; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 231 soluble cytokine class II receptor, short
 FT isoform.
 SQ SEQUENCE 231 AA; 26979 MW; 24A6912BFF75100F CRC64;
 Query Match 15.2%; Score 164.5; DB 2; Length 231;
 Best Local Similarity 27.3%; Pred. No. 2,7e-07;
 Matches 57; Conservative 30; Mismatches 93; Indels 29; Gaps 7;
 QY 9 PONTSLVSTMKRLMWSPIVA--PGETVYVSVEYQGEYSLEYSHINIPSGWCSLTEGPE 67
 DB 31 PQRVQFSRHFHNLQPGALNGSSVYFVQK-----IYGRQKNKEDCGTQEL 85
 QY 68 CDVTDDITATV--PYNLRVATLGSQTSAMSILKHPNRNSTILTRGMEITK-DGFHLV 124
 DB 86 CDLTSE-TSDIQEYVGRVAAASAGSYSEWSTPRTFPMWETKIDPPVNIITVNGSLV 144

QY 125 I-----ELEDLGPQPEFLVAYNRREPGAEHVMYMRSGGI PVHLETMP 168
 DB 145 ILHAPNLPYRYOKKKNVSIID---YVELVRFVFINNSLEKQKVEGARRAIVEALTTP 201
 QY 169 GAAYCYKACQTFVVAIRGRYSAFSGTECEV 197
 DB 202 HSSYCVAAEIVQPLDRSQRSERCVEI 230
 RESULT 7
 ID_1105_MOUSE STANDARD; PRT; 349 AA.
 AC 061190;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
 DE (Cytokine receptor family 2 member 4) (Cytokine receptor class-II
 DE CRF2-4).
 GN Name=110rb; Synonyms=CRFb4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=9719375; PubMed=9047351; DOI=10.1016/S0378-1119(96)00690-7;
 RA Gibbs V.C., Pennica D.;
 RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse
 RT proteins."; [Gene 186:97-101\(1997\)](#).
 RL Gene 186:97-101(1997).
 RN [2]
 RN CHARACTERIZATION.
 RX MEDLINE=98130620; PubMed=9463407;
 RA Spencer S.D., Di Marco F., Hookey J., Pitts-Meek S., Bauer M.,
 RA Ryan A.M., Sordat B., Gibbs V.C., Agnet M.;
 RT "The orphan receptor CRF2-4 is an essential subunit of the interleukin
 RT 10 receptor."; [J. Exp. Med. 187:571-578\(1998\)](#).
 RL J. Exp. Med. 187:571-578(1998).
 CC -1- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain
 CC essential for the active IL10 receptor complex and to initiate
 CC IL10-induced signal transduction events.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
 CC EMBL; U53696; AAC53062.1; -;
 CC MGD; MGI:109380; 110rb.
 DR GO; GO:0004920; F:interleukin-10 receptor activity; IMP.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR Interpro; IPR000282; Cytok_receptor_2.
 DR Interpro; IPR008957; FN_III-like.
 DR PROSITE; PS50853; FN3; 2.
 KM Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 349 Interleukin-10 receptor beta chain.
 FT DOMAIN 20 220 Extracellular (Potential).
 FT TRANSMEM 221 241 Potentia.
 FT DOMAIN 242 349 Cytoplasmic (Potential).
 FT DOMAIN 22 107 Fibronectin type-III 1.
 FT DOMAIN 111 208 Fibronectin type-III 2.
 FT DISUPID 66 74 By similarity.
 FT DISUPID 188 209 By similarity.
 FT CARBOHYD 49 49 N-linked (GlcNAc. . .) (Potential).

DR PIR; A47003; A47003.
 DR HSP; P13726; ITRH.
 DR Genew; HGNC:5965; IL10RB.
 DR H-invDB; HIX0016074; -.
 DR MIM; 123889; -.
 DR GO; GO:0016021; C: integral to membrane; TAS.
 DR GO; GO:0005886; C: plasma membrane; TAS.
 DR GO; GO:0004920; F: interleukin-10 receptor activity; TAS.
 DR GO; GO:0004872; F: receptor activity; TAS.
 DR GO; GO:0006955; P: immune response; TAS.
 DR GO; GO:0006954; P: inflammatory response; TAS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR InterPro; IPR000282; CytoK_receptor_2.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR001187; Tissue_factor.
 DR Pfam; PF01108; Tissue_fac; 1.
 DR Direct protein sequencing; Glycoprotein; Receptor; Signal;
 KW Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 325 Interleukin-10 receptor beta chain.
 FT DOMAIN 20 220 Extracellular (Potential).
 FT TRANSMEM 221 242 Potential.
 FT DOMAIN 243 325 Cytoplasmic (Potential).
 FT DOMAIN 113 205 Fibronectin type-III.
 FT DISULFID 113 205 By similarity.
 FT DISULFID 188 209 By similarity.
 FT CARBOHYD 49 209 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 161 161 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 124 124 A -> D (in Ref. 2).
 FT CONFLICT 269 273 FLAGP -> VGRME (in Ref. 2).
 FT CONFLICT 274 325 Missing (in Ref. 2).
 SQ SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

Query Match 14.8%; Score 159.5; DB 1; Length 325;
 Best Local Similarity 25.7%; Pred. No. 1.2e-06;
 Matches 57; Conservative 37; Mismatches 87; Indels 41; Gaps 12;

QY 3 VALPAPQNSVLTSTNKKHLLMW-SPVLAPEGTYYVSVEYQGESYLSYTHIMIPSSWCS 61
 DB 18 LGWPPPPNVRNMSVNFKNILQWSPAPAKG-----NLTPAQYLSYR-----IFQDKM 67
 QY 62 LTGSPCEDVDITATVPYPLRVATLGSQTSAN-SILKHPFNNSITLTPGCM--BITK 118
 DB 68 NTTLTECDPS-SISKYGDHILRVAFADSHSDMVNITPCV--DDTIIPPGQVAVLA 124
 QY 119 DGFHLVLELDLGPQF-----FLVAYRRBPGEAEHVKVNSGGIPIVH 162
 DB 125 DSLH---KRFAPKLENEYETMTKVVNSWTYVQYMKV--GTDEKFPQITPQYDREV- 177
 QY 163 LETMEPGAAYCVAQTQVKAIGRYSAFSQTECV-VOGEAIP 203
 DB 178 LRNLBPWTTCVQVRGFLPDRNKAGWSEPVCEQTTHDETVP 219

RESULT 10

Q9BUT4 PRELIMINARY; PRT; 325 AA.

AC Q9BUT4; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DB Interleukin 10 receptor, beta.
 GN Name=IL10RB;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahay J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skaleka U., Smallie D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strauberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RA Kolnhe N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Laber J., Lin Y.,
 RA Pheasant M., Farmer A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC001903; AA01903.1; -
 DR EMBL; AY323826; AAP72016.1; -
 DR EMBL; BT009777; AAP8779.1; -
 DR HSP; P13726; ITRH.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004896; F: hemolysate/interferon-class (D200-domain...); IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0007596; P: blood coagulation; IEA.
 DR InterPro; IPR000282; CytoK_receptor_2.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR001187; Tissue_factor.
 DR Pfam; PF01108; Tissue_fac; 1.
 DR SMART; SM00060; FN3; 2.
 KW Receptor.
 SQ SEQUENCE 325 AA; 36995 MW; E470726619AF54C2 CRC64;

Query Match 14.8%; Score 159.5; DB 2; Length 325;
 Best Local Similarity 25.7%; Pred. No. 1.2e-06;
 Matches 57; Conservative 37; Mismatches 87; Indels 41; Gaps 12;

QY 3 VALPAPQNSVLTSTNKKHLLMW-SPVLAPEGTYYVSVEYQGESYLSYTHIMIPSSWCS 61
 DB 18 LGWPPPPNVRNMSVNFKNILQWSPAPAKG-----NLTPAQYLSYR-----IFQDKM 67
 QY 62 LTGSPCEDVDITATVPYPLRVATLGSQTSAN-SILKHPFNNSITLTPGCM--BITK 118
 DB 68 NTTLTECDPS-SISKYGDHILRVAFADSHSDMVNITPCV--DDTIIPPGQVAVLA 124
 QY 119 DGFHLVLELDLGPQF-----FLVAYRRBPGEAEHVKVNSGGIPIVH 162
 DB 125 DSLH---KRFAPKLENEYETMTKVVNSWTYVQYMKV--GTDEKFPQITPQYDREV- 177
 QY 163 LETMEPGAAYCVAQTQVKAIGRYSAFSQTECV-VOGEAIP 203
 DB 178 LRNLBPWTTCVQVRGFLPDRNKAGWSEPVCEQTTHDETVP 219

RESULT 11

Q6ZVU9 PRELIMINARY; PRT; 327 AA.

AC Q6ZVU9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE Hypothetical protein FLJ42063.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.
 RC TISSUE=Synovial membrane tissue;
 RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohara N.,
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
 RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
 RA Kaeriyama S., Sato N., Matsunawa H., Takahashi E., Kataoka R.,
 RA Koga N., Kuroda A., Sato I., Kamata K., Takami S., Terasima Y.,
 RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
 RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
 RA Kikuchi H., Kanda K., Magatsuma M., Murakawa K., Kanehori K.,
 RA Takahashi-Pujji A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK124057; BAC85761.1; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000282; Cytok_receptor_2.
 DR InterPro; IPR008957; FN_III-like.
 KW Receptor.

DR InterPro; IPR008957; FN_III-like.
 KW Receptor.
 SQ SEQUENCE 327 AA; 37430 MW; DACB38F7J12B0EP6 CRC64;

Query Match 14.8%; Score 159.5; DB 2; Length 327;
 Best Local Similarity 25.7%; Pred. No. 1.2e-06;
 Matches 57; Conservative 37; Mismatches 87; Indels 41; Gaps 12;

QY 3 VALIPAPONTLSVLTNMKHLIM-SPVIAGETVYVSEYQGEYSLYTSHIMIPSSWC 61
 DB 20 LGWVPPENVRNMSVNFKNILQWSPFAFG-----NLTTAQLYSR-----IFQDKM 69
 QY 62 LIEGPECDVTDITATVPYNLRVATLGSGTSAM-SILKHPFNKSTILTRPGM--ETK 118
 DB 70 NTLTLECDFS-SISKYGDHTLRVAEPADBSDMVNTTFPCPV--DPTIIGPPGQVEVLA 126
 QY 119 DGFHVLIEEDLGPQPF-----FLVYVMRREPGAEHVMVNSGGIPVH 162
 DB 127 DSIH---MKFLAPKLENEYETWTKMKNVNSWTYVQYWKP--GTDEKFOITPOYDPEV- 179
 QY 163 LETMEPGAAYCAQTFVKAIGRYSAFSQTECWE-VQGEAP 203
 DB 180 LRNLPEFWTYCYVQGRFLPPRNKAGSESPVCEGTHTDERTV 221

RESULT 12
 Q63953 PRELIMINARY; PRT; 332 AA.

AC Q63953;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE Ifngr2 protein (interferon gamma receptor 2).
 GN Name=ifngr2; Synonyms=ifngr2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129SV/U;
 RX MEDLINE=97128072; PubMed=8972742;
 RA Ebersperger C., Rhee S., Muthukumar G., Lembo D., Donnelly R.,
 RA Pestka S., Dembic Z.;
 RT "Genomic organization and promoter analysis of the gene ifngr2
 RT encoding the second chain of the mouse interferon-gamma receptor.";
 RL Scand. J. Immunol. 44:599-606(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boufield G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U69599; AAC52938.1; JOINED.
 DR EMBL; U69594; AAC52938.1; JOINED.
 DR EMBL; U69596; AAC52938.1; JOINED.
 DR EMBL; U69595; AAC52938.1; JOINED.
 DR EMBL; U69597; AAC52938.1; JOINED.
 DR EMBL; U69598; AAC52938.1; JOINED.
 DR EMBL; BC055745; AAC52938.1; JOINED.
 DR PIR; A49947; A49947.
 DR MGI; MGI107654; Ifngr2.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR000282; Cytok_receptor_2.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PSS0853; FN3; 1.
 KW Receptor.
 SQ SEQUENCE 332 AA; 37471 MW; E2DD53BF934BA087 CRC64;

Query Match 14.6%; Score 158; DB 2; Length 332;
 Best Local Similarity 28.8%; Pred. No. 1.7e-06;
 Matches 65; Conservative 29; Mismatches 94; Indels 38; Gaps 14;

QY 1 DEVAIPAPONTLSVLTNMKHLIMSPVIAGETVYVSEYQGEYSLYTSHIMIPSSWC 60
 DB 24 DSFSQALAPLNPRLHYNDQILTWEP--SPSSNDPRPVYQVEYS-----FIDGSMH 74
 QY 61 SLTEGPEC-DVTD--DITR-----TVPYN--LVRATLGSGTSAWSILKHPFNKST 107
 DB 75 RLLE-FNCTDITETKCDLFGGRLKLPFPFTVFLVRKAGNLTSKWGLB--PFOYEN 132
 QY 108 ILTRP--GMEITDGFHVLIEL---DL--GPGFEFLVYVMRREPGAEHVK--MVSGGI 159
 DB 133 VTVGPKNKISVTGKSLVHFSPPPDVHGATFOYLHYHWEKSEFTQOQBOVBGPFKNSI 192

QY 160 PVLHETMEPGAAYCVKAGTFTV---KAIGRYSAFSQTECVYVGEA 201
 DB 193 V--LGNLKPVRVYCLQTEADLILNKKIRPHGLSLNVSCHETTANA 236

RESULT 13

ID Q78EC1 PRELIMINARY; PRT; 332 AA.

AC Q78EC1; 05-JUL-2004 (TREMBlurel. 27, Created)

DT 05-JUL-2004 (TREMBlurel. 27, Last sequence update)

DE Interferon gamma receptor beta subunit.

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10095;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94170381; PubMed=8124717; DOI=10.1016/0092-8674(94)90355-7;
 RA Hammel S., Bohm R., Stark G., Di Marco F., Agnet M.;
 RT "A novel member of the interferon receptor family complements
 RT functionality of the murine interferon gamma receptor in human
 RT cells.";

RL Cell 76:803-810(1994).

DR EMBL; S69336; AAB30165.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR000282; Cytok_receptor_2.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR008957; FN_III-like.

DR Pfam; PF00041; fn3; 1.

DR PROSITE; PSS0853; FN3; 1.

KW Receptor

SQ SEQUENCE 332 AA; 37471 MW; E2DD53BF934BA087 CRC64;

Query Match 14.6%; Score 158; DB 2; Length 332;
 Best Local Similarity 28.8%; Pred. No. 1.7e-06;
 Matches 65; Conservative 29; Mismatches 94; Indels 38; Gaps 14;

QY 1 DEVAILPAPONLSVLTNMKHLMSPVIAAGETVYVSAYQGYSELYSHITIPSSWC 60
 DB 24 DSFSQLAAPNPRLHLVNDQILTWBP--SPSSNDPRPVYQVYVS-----FIDGSM 74

QY 61 SLTEGPEC-DVTD---DITA-----TVPN--LVRATLGSQTSAMSLIKHPFNST 107
 DB 75 RLAE-PVCTDITETKCDLTGGRLKLPHPFTVFLRAKKNLTSKVGLE-PFOHYEN 132

QY 108 ILTRP--GMEITKDGPHLVLEL---DL--GPOEPLVAVWRREPGAEBHYK-MVRSGGI 159
 DB 133 VTYGPPRNISVTGKSLVHFSPRPVPHGATFOYLHNHWEKSETQEQVEGPFKNSI 192

QY 160 PVLHETMEPGAAYCVKAGTFTV---KAIGRYSAFSQTECVYVGEA 201
 DB 193 V--LGNLKPVRVYCLQTEADLILNKKIRPHGLSLNVSCHETTANA 236

RESULT 14

ID Q6UWM1 PRELIMINARY; PRT; 262 AA.

AC Q6UWM1; 05-JUL-2004 (TREMBlurel. 27, Created)

DT 05-JUL-2004 (TREMBlurel. 27, Last sequence update)

DE IL22R2.

OS ORFNames=UNQ5793;

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Baton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson U., Vagte A.,
 RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yamsura D.,
 RA Yi S., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;

RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";

RT Genome Res. 13:2265-2270(2003).

RL EMBL; AY358737; AA089097.1; -

DR HSP; P24055; IIA21.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR InterPro; IPR000282; Cytok_receptor_2.

DR InterPro; IPR008957; FN_III-like.

SQ SEQUENCE 262 AA; 30418 MW; B46BF4DE78ADFDA CRC64;

Query Match 14.0%; Score 151.5; DB 2; Length 262;
 Best Local Similarity 25.0%; Pred. No. 5.3e-06;
 Matches 59; Conservative 32; Mismatches 94; Indels 51; Gaps 8;

QY 9 PNLISVLTNMKHLMSPVIA--PGETVYVSVEYQGYE-SLYTSHIMIPSSW----- 59
 DB 30 PQVVGQFSRPHNHLQWQPRALTGNSVYFVQYKIMFSSMSKSHQKPGCGMHISCNF 89

QY 60 -----CSLTGPECVTDITATV--PNLVRATLGSQTSAMSL 98
 DB 90 PGCRITLAKYQQRWKNKEDCMGTQELSCDLTSE-TSDIQRPYGRVYAAAGSYSEWSMT 148

QY 99 KHPFNKSTLITRPGMEITK-DGFHLY-----LEEDLPQEPFLVAVW 141
 DB 149 PRFTPMWETKIDPPVNMITVNGSLVILHAPNLPRYQEKVNSIED--YELLYRVF 205

QY 142 RRBPGEAEHYKVRSGGI PVLHETMEPGAAYCVKAGTFTVKAIGRYSAFSQTECV 197
 DB 206 IINNSLEKQKVBGAHRAVEIALTPHSSYCVAAEITYQMLDRSGRSERCEVI 261

RESULT 15

ID Q969J5 PRELIMINARY; PRT; 263 AA.

AC Q969J5; 01-DEC-2001 (TREMBlurel. 19, Created)

DT 01-DEC-2001 (TREMBlurel. 19, Last sequence update)

DT 05-JUL-2004 (TREMBlurel. 27, Last annotation update)

DE Soluble cytokine class II receptor, long isoform precursor
 DE (Interleukin 22-binding protein CRP2-10L).

GN Name=CRP2-S1; Synonyms=IL22BP;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE=Placenta;

RX MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sg.gene.6363786;
 RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toechi L., Kunz S.,
 RA Wolk K., Asadullah K., Sabat R.;

RT "A novel, soluble homologue of the human IL-10 receptor with
 RT preferential expression in placenta.";

RL Genes Immun. 2:329-334 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21286453; PubMed=11390454;
 RA Kotenko S.V., Izkotova L.S., Mitrochitchenko O.V., Basterova E.,
 RA Dickenhaeet H., Donnelly R.P., Pestka S.,
 RT "Identification, cloning, and characterization of a novel soluble
 RT receptor that binds IL-22 and neutralizes its activity.";

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RL J. Immunol. 166:7096-7103(2001).
DR EMBL; AJ313162; CAC85635.1; -.
DR EMBL; AY040567; AAK85715.1; -.
DR HSRP; P24055; 1A21.
DR Genew; HGNC:14901; IL22RA2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR008957; FN_III-like.
KW Receptor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 263 soluble cytokine class II receptor, long
FT isoform.
SQ SEQUENCE 263 AA; 30550 MW; C96EGCSD78AC79B CRC64;

Query Match 14.0%; Score 151.5; DB 2; Length 263;
Best Local Similarity 25.0%; Pred. No. 5.3e-06;
Matches 59; Conservative 32; Mismatches 94; Indels 51; Gaps 8;

QY 9 PONTSLSTNMKHLMMSPVIA-PGETVYYSVEYQGEYE-SLYTSHIWIPSSW----- 59
DB 31 PQRVQPSRNFHNLQMPGRALTNSSVYFQYKIMFSCSMKSSHQKRGCMQHISCNF 90
QY 60 -----CSLTGPECCVTDITATV--PYNLRVYRATLGSQTSAMSI 98
DB 91 PGCRTLAKYGQROWKNKEDCWGTQELSCDLTSE-TSDIQEPYGRVRAASAGSYSEWSMT 149
QY 99 KHPFNKNSLTILTPGHEITK-DGFHLVI-----ELEDLGPQFEFLVAYW 141
DB 150 PRFTPMWETKIDPPVNMITQVNGSLVILHAPNLPRYQREKKNVSIED--YVELLYRVF 206
QY 142 RREPGEAEHYKAVRSQGI PVHLETMERGAAYCVKACTFVKAIGRYSAFSQTECEV 197
DB 207 IINNSLEKEQKVEGAHRAVEIALTPHSSYCVVAELIYQPMIDRRSGRSEERCEI 262

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Search completed: February 25, 2005, 02:43:36
 Job time : 109.724 secs

GenCore version 5.1.6
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OM proteoln - protein search, using sw model

Run on: February 25, 2005, 02:24:39 ; Search time 117.276 Seconds
(without alignments)
964.985 Million cell updates/sec

Title: US-09-745-792a-12
Perfect score: 1200
Sequence: 1 VPCVSGGLPKPANITPLSLN.....PSEKQCARILKDGSSSEPKAK 221

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_tr embl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1200	100.0	553	1	Q9UHT4 homo sapien
2	965	80.4	546	1	Q6PHD0 mus musculi
3	888.5	74.0	209	2	Q96SH7
4	336	28.0	231	2	Q96A41
5	333.5	27.8	568	2	Q800P7
6	333.5	27.8	568	2	Q800G1
7	315	26.2	229	2	Q7TNI4
8	310	25.8	263	2	Q6UWM1
9	310	25.8	263	2	Q969J5
10	277	23.1	230	2	Q7TNI5
11	275	22.9	230	2	Q80XFS
12	264.5	22.0	341	2	Q9YGC8
13	233.5	19.5	327	2	Q6ZVU9
14	232.5	19.4	325	1	I10S_HUMAN
15	232.5	19.4	325	2	Q9BUT4
16	229.5	19.1	349	1	I10S_MOUSE
17	229.5	19.1	362	2	Q764M7
18	226.5	18.9	338	2	Q800G2
19	223.5	18.6	336	2	Q800E8
20	223	18.6	351	2	Q8VHM7
21	221	18.4	130	2	Q96GRO
22	204	17.0	203	2	Q7ZT05
23	204	17.0	442	2	Q9PVU9
24	202	16.8	569	2	Q9YHMO
25	196	16.3	530	1	INR1_MOUSE
26	196	16.3	530	2	Q80UJ3
27	196	16.3	530	2	Q80UR8
28	194	16.2	333	2	Q7ZTJ0
29	192.5	16.0	574	2	Q8N6P7
30	192.5	16.0	574	2	Q9H8Z2
31	190	15.8	305	2	Q6DCU5

32	187	15.6	560	2	Q764M8	Q764M8 sus scrofa
33	186.5	15.5	560	1	INR1_BOVIN	Q04750 bos taurus
34	183	15.2	581	2	Q80XZ4	Q80XZ4 mus musculi
35	177.5	14.8	284	2	Q7ZT22	Q7ZT22 tetraodon n
36	168.5	14.0	557	1	INR1_HUMAN	P17181 homo sapien
37	167.5	14.0	301	2	Q7ZT35	Q7ZT35 tetraodon n
38	166.5	13.9	332	2	Q9GK86	Q9GK86 ovis aries
39	166.5	13.9	387	2	Q6PKD7	Q6PKD7 homo sapien
40	166.5	13.9	557	2	Q8WT22	Q8WT22 homo sapien
41	166.5	13.9	560	1	INR1_SHEEP	Q28589 ovis aries
42	163.5	13.6	489	1	INR1_HUMAN	P15260 homo sapien
43	162	13.5	289	1	TP_CAVPO	Q9J1J8 cavia porce
44	161.5	13.5	489	2	Q9B769	Q9B769 homo sapien
45	159.5	13.3	294	2	Q90W13	Q90W13 oncorhynchus

ALIGNMENTS

RESULT 1
ID 120R_HUMAN STANDARD; PRT; 553 AA.
AC Q9UHT4; Q6UW49; Q96SH8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Interleukin-20 receptor alpha chain precursor (IL-20R-alpha) (IL-20R1)
DE (ZCYTOR7) (Cytokine receptor family 2 member 8) (CRR2-8)
DE (UNO681/PRO1315).
GN Name=IL20RA; Synonyms=ZCYTOR7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
RA Lok S., Kho C., Jellmberg A., Adams R., Whitmore T., Parrish T.,
RA O'Hara P.;
RT "Homo sapiens cytokine receptor homolog.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Ginaldi C., Gu O., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simone L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashure J.L.,
RA Wilmshill A.J., Jones M.C., Horton R., Hunt S.E., Scott C.B.,
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Alnough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA Babbage A.K., Bagunley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown Y.Y.,
RA Burford D.C., Burrill I.W., Burton J., Carter C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Cullay K.M., Dhami P., Davies J., Dunn M., Barthow M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French J., Garner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gillison C.J., Githero R.J., Grahame D.V., Grant M.,

RA Griddle S., Griffiths C., Griffiths M.N.D., Hall R., Halle K.S.,
RA Hammond S., Hawley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leonardornier D.A., Leverhna M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Matthews L., McMan O.T., McLaren S.J., McKay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.U.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Raby S.A., Rice C.M., Rose M.T., Seaton L.,
RA Seta H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.,
RT "The DNA sequence and analysis of human chromosome 6.",
RL Nature 425:805-811(2003).
[4]
RP SEQUENCE OF 30-44.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RL verified cleavage sites".
RL Protein Sci. 13:2819-2824(2004).
[5]
RN SUBUNIT, LIGAND BINDING, AND TISSUE SPECIFICITY.
RP MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
RX Lumberg H., Conklin D., Xu W.F., Groseman A., Brenden T.,
RA Carollo S., Eagan M., Foster D., Haldeman D., Hammond A., Hangan H.,
RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Season S., Sprecher C., Magye K., West J.,
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.,
RT "Interleukin 20: discovery, receptor identification, and role in
RL epidermal function".
RL Cell 104:9-19(2001).
[6]
RN LIGAND BINDING.
RP PubMed=11564763;
RX Dumoutier L., Leemans C., Lejeune D., Kotenko S.V., Renaud J.-C.,
RT "STAR activation by IL-19, IL-20 and mda-7 through IL-20 receptor
RL complexes of two types".
RL J. Immunol. 167:3545-3549(2001).
[7]
RN SUBUNIT, AND LIGAND BINDING.
RP PubMed=12351624; DOI=10.1074/jbc.M205114200;
RX Parrish-Novak J., Xu W., Brenden T., Yao L., Jones C., West J.,
RA Brandt C., Jelinek L., Madden K., McKernan P.A., Foster D.C.,
RA Jaspers S., Chandrasekhar Y.A.;
RT "Interleukins 19, 20, and 24 signal through two distinct receptor
RT complexes. Differences in receptor-ligand interactions mediate unique
RT biological functions".
RL J. Biol. Chem. 277:47517-47523(2002).
[8]
RN SUBUNIT, AND LIGAND BINDING.
RP PubMed=14580208; DOI=10.1021/bi0354583;
RX Pietner S., Magracheva E., Kozlov S., Tobin G., Kotenko S.V.,
RA Wlodawer A., Zdanov A.;
RT "Characterization of the recombinant extracellular domains of human
RT interleukin-20 receptors and their complexes with interleukin-19 and
RT interleukin-20".
RL Biochemistry 42:12617-12624(2003).
[9]
RN SUBUNIT, LIGAND BINDING, AND TISSUE SPECIFICITY.
RP PubMed=14764663;
RX Sheith F., Baurin V.V., Lewis-Antes A., Shah N.K., Smirnov S.V.,
RA Ananba S., Dickenshefts H., Dumoutier L., Renaud J.C., Zdanov A.,
RA Donnelly R.P., Kotenko S.V.;
RT "IL-26 signals through a novel receptor complex composed of IL-20
RT receptor 1 and IL-10 receptor 2.";

RL J. Immunol. 172:2006-2010(2004).
CC -1- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20 and
CC IL24. The IL20RA/IL20RB dimer is a receptor for IL26.
CC -1- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL10RB.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UHF4-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UHF4-2; Sequence=VSP_011497, VSP_011498;
CC TISSUE SPECIFICITY: Widely expressed with highest levels in skin
CC and testis and high levels in brain. Highly expressed in psoriatic
CC skin.
CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF184971; AA091320.1; -;
CC EMBL; AY358883; AA089242.1; -;
CC EMBL; AL135902; CAC38375.1; -;
CC HSSP; P13726; 2HPT.
CC Genew; HGNC:6003; IL20RA.
CC MIM; 605620; -;
CC InterPro; IPR000282; Cytok_receptor_2.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR001187; Tissue_factor.
CC Pfam; PF01108; Tissue_fac; I.
CC DR PROSITE; PS0053; FN3; FALSE_NEG.
CC KX Alternative splicing; Direct protein sequencing; Glycoprotein;
CC Receptor; Repeat; Signal; Transmembrane.
CC
CC FT SIGNAL 1 29
CC FT CHAIN 30 553 Interleukin-20 receptor alpha chain.
CC FT DOMAIN 30 250 Extracellular (Potential).
CC FT TRANSMEM 251 271 Potential.
CC FT DOMAIN 272 553 Cytoplasmic (Potential).
CC FT DOMAIN 37 136 Fibronectin type-III 1.
CC FT DOMAIN 138 237 Fibronectin type-III 2.
CC FT DOMAIN 353 356 Poly-Glu.
CC FT DISULFID 67 95 By similarity.
CC FT DISULFID 215 236 By similarity.
CC FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 83 83 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 91 91 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 191 191 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
CC FT VARSPLIC 1 111 Missing (in isoform 2).
CC FT VARSPLIC 112 135 FTId=VSP_011497.
CC FT VARSPLIC 135 135 VKAIGTCKSWAESGRFPFLPT -> MSYNGLHORVPE
CC FT LKLTICGIS (in isoform 2).
CC FT CONFLICT 259 259 FTId=VSP_011498.
CC FT CONFLICT 382 382 I -> V (in Ref. 2).
CC FT CONFLICT 382 382 F -> L (in Ref. 2 and 3).
CC SQ SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;
Query Match 100.0%; Score 1200; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 7.9e-100; Indels 0; Gaps 0;
Matches 221; Conservative 0; Mismatches 0;
QY 1 VPCVGGSLPKPANIFLSINMKNVLTQWTPPEGLQGVKTYTYQYFITYGCKMLNKSCKRN 60
DB 30 VPCVGGSLPKPANIFLSINMKNVLTQWTPPEGLQGVKTYTYQYFITYGCKMLNKSCKRN 89
QY 61 INRTYCDLSAETSDYEHQYAKVKAIWGTCKSWAESGRFPFLPTQIGPPVALTTDEK 120

DB 90 INRTYCDLSAETSDYEHQYAKYKAIWGTCKSKMAESGRYPPLFETQIGPEVALTTDEK 149
QY 121 SISVLTAPBEKWRNPEDLPVSMQOYISNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 180
DB 150 SISVLTAPBEKWRNPEDLPVSMQOYISNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 209
QY 181 PNTLYCVHVESFVPGPPRRAPQSEKOCARTLKXOSSSEFPK 221
DB 210 PNTLYCVHVESFVPGPPRRAPQSEKOCARTLKXOSSSEFPK 250

RESULT 2
12OR_MOUSE STANDARD; PRT; 546 AA.
ID 12OR_MOUSE
AC 06PHE0; 06BWE4;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-20 receptor alpha chain precursor (IL-20R-alpha) (IL-20R1).
GN Name=120ra;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; PubMed=12466851; DOI=10.1038/nature01266;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Nikaido I., Furuno M., Kankawa T., Adachi J., Bono H., Kondo S., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gotohori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schirral L.M., Kanpin A., Matsuda H., Batalov S., Balise K.W., Blake J.A., Bradt D., Brucic V., Chothia C., Corbani L.B., Cousins S., Dalia E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S., Gaubertand T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Guinlich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H., Nagahima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Raveli T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynnaw-Boris A., Yamagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shitake T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hoshitume K., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Breast tumor;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F., Diatchenko L., Matsuda K., Farmer A.A., Rubin G.M., Hong L., Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange S., Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mulhany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Huik S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyzanski M.I., Skalka U., Smallie D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., RT "generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL26 and IL24. The IL20RA/IL20RB dimer is a receptor for IL26 (By similarity).
CC -1- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL10RB (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
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CC EMBL; AK054215; BAC35695.1; -;
CC EMBL; BC056628; AAH56628.1; -;
CC HSSP; P13726; 2HPT.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR001187; Tissue_factor.
DR Pfam; PF01108; Tissue_fac; I.
DR PROSITE; PS05853; FN3; PALSE. NEG.
KM Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 32
FT CHAIN 33 546
FT DOMAIN 33 253
FT TRANSMEM 254 274
FT DOMAIN 275 546
FT DOMAIN 33 142
FT DOMAIN 143 251
FT DISULFID 90 98
FT DISULFID 218 239
FT CARBOHYD 45 45
FT CARBOHYD 86 86
FT CARBOHYD 94 94
FT CARBOHYD 185 185
FT CARBOHYD 203 203
FT CONFLICT 145 145
SQ SEQUENCE 546 AA; 61977 MW; E7EC07DA2D49A7F CRC64;
Query Match 80.4%; Score 965; DB 1; Length 546;
Best Local Similarity 79.6%; Pred. No. 1,4e-78;
Matches 176; Conservative 15; Mismatches 30; Indels 0; Gaps 0;
QY 1 VPCVSGGLPKNATITFSLNMKNVLTQTEPGLQGVKVTYQYFYGOKMKNKSCRN 60
DB 33 VPCVSGGLPKNATITFSLNMKNVLTQTEPGLQGVKVTYQYFYGOKMKNKSCRN 92
QY 61 INRTYCDLSAETSDYEHQYAKYKAIWGTCKSKMAESGRYPPLFETQIGPEVALTTDEK 120
DB 93 INRTYCDLSAETSDYEHQYAKYKAIWGTCKSKMAESGRYPPLFETQIGPEVALTTDEK 152
QY 121 SISVLTAPBEKWRNPEDLPVSMQOYISNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 180
DB 153 SISVLTAPBEKWRNPEDLPVSMQOYISNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 212
QY 181 PNTLYCVHVESFVPGPPRRAPQSEKOCARTLKXOSSSEFPK 221
DB 213 PNTLYCVHVESFVPGPPRRAPQSEKOCARTLKXOSSSEFPK 253

```
RESULT 3
O66SH7 PRELIMINARY; PRT; 209 AA.
ID O96SH7
AC O96SH7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BA204P2.1.3 (Interleukin 20 receptor alpha, isoform 3).
GN Name:IL20RA,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Griffiths C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ135902; CAC38376.1; -.
DR HSSP; P13726; 2HFT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR008957; FN_III-like.
KM Receptor.
SQ SEQUENCE 209 AA; 23616 MW; 467AB77BE3840361 CRC64;

Query Match 74.0%; Score 888.5; DB 2; Length 209;
Best Local Similarity 90.5%; Pred. No. 3,4e-72;
Matches 171; Conservative 1; Mismatches 4; Indels 13; Gaps 3;

QY 1 VPCVSGGLPKPANITFLSTINKKVLQWTPPEGLQGVKVTYVQYFYIGQKKMLKSECKN 60
DB 30 VPCVSGGLPKPANITFLSTINKKVLQWTPPEGLQGVKVTYVQYFYIGQKKMLKSECKN 89
QY 61 INRTYCDLSAETSDYEHQYAKYKAIWGTCKSKMAESGRFPFLETOIGPEVALTTDEK 120
DB 90 INRTYCDLSAETSDYEHQYAKYKAIWGTCKSKMAESGRFPFLETOIGPEVALTTDEK 149
QY 121 STSVLTAPPKMKRNPEDLPVSMQOQYSLNKNVSVLNTKSNRTWQCVTNHTLVLTWLE 180
DB 150 STSVLTAPPKMKRNPEDLPVSMQOQYSLNKNVSVLNTKSNRTWQCVTNHTLVLTWLE 198
QY 181 PNTLYCVHV 189
DB 199 -NGAY- IHV 205

RESULT 4
O96A41 PRELIMINARY; PRT; 231 AA.
ID O96A41
AC O96A41;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Soluble cytokine class II receptor, short isoform precursor
DE (Interleukin 22-binding protein CRP2-10) (Class II cytokine receptor)
DE (IL22RA2).
GN Name-CRP2-S1; Synonyms=IL-22BP, IL22BP, IL22RA2; ORNames=UNQ5793;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Mammary gland;
RA MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sj.gene.6363786;
RA Guenbery B.H., Schoenemeyer A., Weiss B., Toschl L., Kunz S.,
RA Wolk K., Asadullah K., Sabat R.;
RT "A novel, soluble homologue of the human IL-10 receptor with
RT preferential expression in placenta.";
RN [2]
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RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Dumoutier L., Lejeune D., Renaud J.C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RX Kotenko S.V., Izotova L.S., Mitrochitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RT "Identification, cloning, and characterization of a novel soluble
RT receptor that binds IL-22 and neutralizes its activity.";
RL J. Immunol. 166:7096-7103(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396522; PubMed=11481447; DOI=10.1073/pnas.171303198;
RX Xu W., Frennell S.R., Parrish-Novak J., Kinsvogel W., Jaspers S.,
RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schultemeyer S.,
RA Yao L., Whitmore T.E., Chandrasekhar Y., Grant F.D., Maurer M.,
RA Jelinek L., Storey H., Bender T., Hammond A., Topouzis S.,
RA Clegg C.H., Foster D.C.;
RT "A soluble class II cytokine receptor, IL-22RA2, is a naturally
RT occurring IL-22 antagonist.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.129303;
RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Devel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RL EMBL; AJ31161; CAC86534.1; -.
DR EMBL; AJ297262; CAC83097.1; -.
DR EMBL; AY040566; AAK85714.1; -.
DR EMBL; AY044429; AAK91775.1; -.
DR EMBL; AY358111; AAO88478.1; -.
DR HSSP; P24055; 1A21.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR008957; FN_III-like.
KW Receptor; Signal.
FT SIGNAL 1 21 potential.
FT CHAIN 22 231 soluble cytokine class II receptor, short
FT isoform.
SQ SEQUENCE 231 AA; 26979 MW; 24A6912BFF75100F CRC64;

Query Match 38.0%; Score 336; DB 2; Length 231;
Best Local Similarity 37.2%; Pred. No. 3,5e-22;
Matches 74; Conservative 33; Mismatches 90; Indels 2; Gaps 2;

QY 10 KPANITFLSINKKVLQWTPPEGLQGVKVTYVQYFYIGQKKMLKSECKNINRTYCDLS 69
DB 30 KPANITFLSINKKVLQWTPPEGLQGVKVTYVQYFYIGQKKMLKSECKNINRTYCDLS 89
QY 70 AETSDYEHQYAKYKAIWGTCKSKMAESGRFPFLETOIGPEVALTTDEKSISVTLAP 129
DB 90 AETSDYEHQYAKYKAIWGTCKSKMAESGRFPFLETOIGPEVALTTDEKSISVTLAP 149
QY 130 EKKKNPEDLPVSMQOQYSLNKNVSVLNTKSNRTWQCVTNHTLV-LTWLEPNTLYCVH 188
DB 150 NLPFYQKEKIVSIDY-ELLYKVFIIINSLEKQKYEGHRAVEIALTPHSYCV 208
QY 189 VESFVGPFPRAQPSKOC 207
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Db 209 AETVQPMDBRRSQRSEBRC 227

RESULT 5

Q800F7

PRELIMINARY;

PRT; 568 AA.

ID Q800F7

01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DB Helical cytokine receptor CRFB8.

GN Name=crfb8;

Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OK NCBI_TaxId=99883;

RN (1)

RP SEQUENCE FROM N.A.

RA Lutfalla G., Roest Crolius H., Strange-Thomann N., Jallion O.,

RA Mogensen K., Monneron D.;

RT "Comparative genomic analysis reveals independent expansion of a

RT lineage-specific gene family in vertebrates: The class II cytokine

RT receptors and their ligands in mammals and fish."

RL BMC Genomics 4:29-29(2003).

DR EMBL; AJ544894; CAD67782.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR000282; Cytok_receptor_2.

DR InterPro; IPR008957; FN_III-like.

KW Receptor.

SQ SEQUENCE 568 AA; 63848 MW; ABA38DCB3F78ABE2 CRC64;

Query Match 27.8%; Score 333.5; DB 2; Length 568;

Best Local Similarity 33.8%; Pred. No. 1.8e-21;

Matches 75; Conservative 41; Mismatches 87; Indels 19; Gaps 4;

4 VSGGLPKPANITFLSINMKVLTQWTPPEGLQGVKVTYTYGYGQK-----KWLKSE 57

16 VSASLPSPTSVFASVNLRLVLEWTPGNDTPS-NATFTQYALYGDSDKRSVWMAIOR 74

58 CRINNTYCDLSAETSDYEHQYAKYKAIWGTGCSKMABSGRYPFLETOIGPEVALTT 117

75 CINTAOSKCDLSNQTDLEBAYARARASRKAMSGSOTRRDPKSDITFGPPQMSVEV 134

118 DEKSIISVLTAPPEKWRNPEDLPVSMQOITYSNLKYNVSVLNTKSNRTWSQCVNHTLVLT 177

135 ENSNAIVTVKGPMPRYQPNQMPAVSMATYIPHMVNLSTINTYRNK-----TSHPISS 188

178 WL-----EPNTLYCYHVESFVPGPPRAOPSEKQCARLTKD 213

189 GLYKHLALRYNKYCFPSYAKFLAMPVQCQSSSEMOCITTPTD 230

Db 189 GLYKHLALRYNKYCFPSYAKFLAMPVQCQSSSEMOCITTPTD 230

RESULT 6

Q800G1

PRELIMINARY;

PRT; 568 AA.

ID Q800G1

01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DB Helical cytokine receptor CRFB8.

GN Name=crfb8;

Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OK NCBI_TaxId=99883;

RN (1)

RP SEQUENCE FROM N.A.

RA Lutfalla G., Roest Crolius H., Strange-Thomann N., Jallion O.,

RA Mogensen K., Monneron D.;

RT "Comparative genomic analysis reveals independent expansion of a

RT lineage-specific gene family in vertebrates: The class II cytokine

RT receptors and their ligands in mammals and fish."

RL BMC Genomics 4:29-29(2003).

DR EMBL; AJ544894; CAD67782.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR000282; Cytok_receptor_2.

DR InterPro; IPR008957; FN_III-like.

KW Receptor.

SQ SEQUENCE 568 AA; 63834 MW; FE3AA901C0C31B93 CRC64;

Query Match 27.8%; Score 333.5; DB 2; Length 568;

Best Local Similarity 33.8%; Pred. No. 1.8e-21;

Matches 75; Conservative 41; Mismatches 87; Indels 19; Gaps 4;

4 VSGGLPKPANITFLSINMKVLTQWTPPEGLQGVKVTYTYGYGQK-----KWLKSE 57

16 VSASLPSPTSVFASVNLRLVLEWTPGNDTPS-NATFTQYALYGDSDKRSVWMAIOR 74

58 CRINNTYCDLSAETSDYEHQYAKYKAIWGTGCSKMABSGRYPFLETOIGPEVALTT 117

75 CINTAOSKCDLSNQTDLEBAYARARASRKAMSGSOTRRDPKSDITFGPPQMSVEV 134

118 DEKSIISVLTAPPEKWRNPEDLPVSMQOITYSNLKYNVSVLNTKSNRTWSQCVNHTLVLT 177

135 ENSNAIVTVKGPMPRYQPNQMPAVSMATYIPHMVNLSTINTYRNK-----TSHPISS 188

178 WL-----EPNTLYCYHVESFVPGPPRAOPSEKQCARLTKD 213

189 GLYKHLALRYNKYCFPSYAKFLAMPVQCQSSSEMOCITTPTD 230

Db 189 GLYKHLALRYNKYCFPSYAKFLAMPVQCQSSSEMOCITTPTD 230

RESULT 7

Q7TN14

PRELIMINARY;

PRT; 229 AA.

ID Q7TN14

01-OCT-2003 (TREMBlrel. 25, Created)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DB Cytokine receptor family II soluble 1 precursor.

GN Name=crf2-61;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxId=10116;

OK (1)

RN SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Spleen;

RA Weiss B., Volk K., Gruenberg B.H., Volk H.D., Sterry W., Asadullah K.,

RA Sabat R.;

RT "Cloning of murine IL-22 receptor alpha 2 and comparison with its

RT human counterpart."

RL Genes Immun. 5:330-336(2004).

DR EMBL; AJ555485; CAD88475.1; -.

DR HSSP; P13726; IJPS.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR000282; Cytok_receptor_2.

DR InterPro; IPR008957; FN_III-like.

KW Receptor; Signal.

FT SIGNAL

PT CHAIN

SQ SEQUENCE 229 AA; 26721 MW; SCFEDJ37652A9365 CRC64;

21 229 cytokine receptor family II soluble 1.

Query Match	26.2%	Score 315	DB 2	Length 225
Best Local Similarity	34.5%	Pred. No. 2.7e-20		
Matches	70	Conservative 30	Mismatches 97	Indels 6
			Gaps 3	
QY	10	KEANITFLSLNNKNVLTOWTPPEGLQGVKTYTYVPEIYIGQCKWLANKSECRNIRTYCDLS	69	
DB	28	KPKQVQSGRPNHNLHWQPGNSLTNGSVTVFYQVYTKYGGQWKDKNDGCTALFCDDL	87	
QY	70	AETSYEHQYAKYKAIWGTCKSKAASEGRFPFLETOGPREVALITBTEKSLSVLITAP	129	
DB	88	KETLPDYEBYGRVMMAMAGSYSEWRTFRFTPMWETKLDPPVYITITRVNASLRYLRBP	147	
QY	130	EKKRNKPEDLPVSMOOIYSNLKYNVSLNT---KSNRTYSQCVTNHTLVLTWLDEPTLYC	186	
DB	148	ELPHNNQGGKNTSMENYV-NLYVRYSIINNSLEKEQKAYEG--TQNAVETIGLTPHCSTC	204	
QY	187	VHVESFVQPPRRAPDSEKQCAR	209	
DB	205	VVAEMYQPFDRRSPRSKERCVO	227	

RESULT	8			
06UWM1		PRELIMINARY;	PRT;	262 AA.
ID	06UWM1			
AC	06UWM1;			
DT	05-JUL-2004 (TREMBlrel. 27, Created)			
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)			
DE	1122R82.			
GN	ORFNames=UNO5793;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Raeton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark W., Robble E., Sanchez C., Schoenfeld J.,			
RA	Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
DR	EMBL; AY358737; AAC09097.1; -.			
DR	HSSP; P24055; 1A21.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0046896; F:hematopoietin/interferon-class (D200-domain.. .; I			
DR	InterPro; IPR000282; Cytok_receptor_2.			
DR	InterPro; IPR008957; FN_III-like.			
SO	SEQUENCE 262 AA; 30418 MW; E46EEF4DE79ADFDA CRC64;			

	Query Match	25.8%	Score 310;	DB 2;	Length 262;
	Best Local Similarity	32.0%;	Pred No.	9e-20;	
	Matches	74;	Conservative	33;	Mismatches 90; Indels 34; Gaps 3
OY	10	KPANIITPLSINKNVYLQWTPREGLOGVKVTYYGYFI-----	46		
Db	29	KFORVOFSRNMHNILIQOPGRALTGNSSVFYQYIMFSCMSKSHQPSGCMOHSICN	88		
OY	47	-----YGGKMVLNKSECCNINRTCDLSAETSDVEHOYAYKAMWGKCSKMAES	97		
Ddb	89	FPGCCTLAKTGOROKMKMEDCWGTGLBELSCDLSIFTSIDLOEPFYRGKRASAGSYEMSWTT	148		
OY	98	GHPYFPLELTQIGPEVALTTDEKSISSVVLTADEKKRNRPEDLPVSQQIYSMLKTVNVSL	157		

Db 149 PRFTPMWEKIDBPVMMNTITQVNGSLVILHAPNLEPRYQKKNVSIEDY-ELLTRYFII 207

QY 158 NTSNRTWQCVTNHTLV-LTWLEPNLTLCYHVESFVPGGPRRQKQSEKOC 207

Db 208 MNSLEKQKVTGSAHRAVEITLTHSSCYVAALTYQPMIDRNSQREBK 258

RESULT 9				
096935				
ID	096935	PRELIMINARY;	PRF;	263 AA.
AC	Q96935;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Soluble cytokine class II receptor, long isoform precursor			
DE	(Interleukin 22-binding protein CRF2-10L).			
GN	Name=CRF2-SI; Synonyms=IL22BP;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Carnivora; Hominiina; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MELLINE=J1518574; PubMed=11607789; DOI=10.1038/sj.gene.6363786;			
RA	Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,			
RA	Molk K., Aesdullah K., Sabot R.,			
RT	"A novel, soluble homologue of the human IL-10 receptor with			
RL	preferential expression on placenta.";			
RL	Genes Immun. 2:329-334(2001).			

RP	SEQUENCE FROM N.A.
RX	MEDLINE=21286453; Pubmed=11390454;
RA	Kichenko S.V., Iotova L.S., Mirochnitchenko O.V., Beterova E.,
RB	Dikensheets H., Donnelly R.P., Peetka S.;
RT	"Identification, Cloning, and characterization of a novel soluble
RT	receptor that binds IL-22 and neutralizes its activity." ;
RL	J. Immunol. 166:7096-7103(2001).
DR	EWBL; AJ313162; CAC85635.1; -.
DR	EWBL; AY040567; AAK85715.1; --.
DR	HSSP; P24055; 1A21.
DR	Genew; HGNC:14901; IL22RA2.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0004886; F:hematopoietin/interferon-class (D200-domain..); IEA
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPRO00282; CytoK receptor _2.
DR	InterPro; IPRO08957; FN_III-like.
KW	Receptor; Signal.
FT	SIGNAL
FT	CHAIN
FT	22
FT	21
FT	Potential.
FT	soluble cytokine class II receptor, long
FT	isoform.
SEQ	SEQUENCE 263 AA; 30550 MW; G96EECECD78AC79B CRC64;

	Query Match	25.8%	Score 310;	DB 2;	Length 263;	
	Best Local Similarity	32.0%	Pred. 9.1e-20;			
	Matches	74;	Conservative	33;	Mismatches	90;
					Indels	34;
					Gaps	3
<hr/>						
Qy	10	KPANIITFLSNMKVQLQWTPPEGLQGVKVTYVQYFI-----	46			
Db	30	KPQVVOFQSRFRHNLQWQFGRALTGNSSVYFVQYIKFSCSMKSHQKPSGCMOHISCN	89			
Qy	47	-----YQCKMLKSECRNINRTYCDLSAEFSQVHENQYIAVKVLIWGTGSKMAES	97			
Db	90	PPGCRITLAKYQQRQWKNEDECMGTQOELSCDILTSETSDIQEPYLVGVRAASAGSYSEMSKT	149			
Qy	98	GRFPYFLETQIGPPEVALTTDEKISIVLITAPAEKKRNRPEDLPVSMQOIVSNLKYVAVL	157			
Db	150	PRFPFMWETKIDPVPVNNITQVNGSLVLIHAHPNLPYRQGEKQNVSIEDDY-ELLYRVFII	208			
Qy	158	NTKSNRTWSQCVNTHILV-LTWLEBNPILCYHVSFVVGPPRRAPQSEKQC	207			
Db	209	NNSLEKDEKVEGAHRAVEIALTPHSSYCVAAELTYQOMLRRSGRSEERC	259			


```
DR PRINTS; PR00346; TISSUEFACTOR.
DR SMART; SMO0060; FN3; 2.
DR PROSITE; PS00853; FN3; 1.
KW Receptor.
SQ SEQUENCE 341 AA; 39062 MW; 18027239BFA9C87 CRC64;

Query Match
Best Local Similarity 32.4%; Score 264.5; DB 2; Length 341;
Matches 70; Conservative 43; Mismatches 80; Indels 23; Gaps 9;

QY 3 CYSGLPKRANITFLSINKNVLQTPPEGLQGVKTYVQ-YFLYGQKMLINKSCRN 61
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 16 CYSGLVPRKRNARISSVNFRSVLMDPP-GVRKGNISLYVQAKSIFPKQNFNNVT--TWL 72
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 62 NRTYCDLSAETSDYEHQYAKVKAIVGTGCSKMAESGRFPYLETOIGPPEVALTTDEKS 121
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 73 NVTEDCVSS-LSVY-GAYLVKRVTEWEDSHDAVV-RKRPADTYIGPSPVNVSESGT 129
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 122 ISVVLTPA-----EKMKNPEDLPVSMQOISNLKYNVSVLNTKSNRTWSQCVTNH-TL 174
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 130 LHVDFTPGPADEHDKM-----SLKQYGSWYRLLYWKGSNKKVTHIDTKHNS 180
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 175 VLTWLEPNTLYCVHVESFVPGPPRAQPSKOCART 210
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 181 ILSQLEPWTICYIQVGVIPENWKTGERSQELCEQT 216
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13
Q6ZVU9 PRELIMINARY; PRT; 327 AA.
AC 06ZVU9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Hypothetical protein FLJ42063.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Synovial membrane tissue;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba B., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsumura H., Takahashi E., Katoaka R.,
RA Kuga N., Kuroda A., Satoh I., Kamaya K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Isono Y., Otsuki T., Sato H., Wakamatsu A.,
RA Ishii S., Yamamoto J., Ito Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Pujji A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK124057; BAC85761.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin;interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR008957; FN_III-like.
KW Receptor.
SQ SEQUENCE 327 AA; 37430 MW; DACB38F7312B0EF6 CRC64;

Query Match
Best Local Similarity 29.2%; Score 233.5; DB 2; Length 327;
Matches 63; Conservative 36; Mismatches 94; Indels 23; Gaps 6;

QY 6 GGLPKRANITFLSINKNVLQTPPEGLQGVKTYVQYFIYGQKMLINKSCRNIRTY 65
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 21 GWPPEPBNVAMSVNFKNIQWSPAFAG-NLFTAQVLSYR---IFPDKCNLTITTE 75
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 66 CDLSAETSDYEHQYAKVKAIVGTGCSKMAESGRFPYLETOIGPPEVALTTDEKSISV 125
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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DB 76 CDFSSLSKYGCHT--LRVRAEPADSHSDPVANI-TFCPVDDITIGPPGMQVEVLADSLMR 132
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 126 LTAP-----EKMKNPEDLPVSMQOISNLKYNVSVLNTKSNRTWSQCVTNHTLVTWL 179
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 133 FLAPKIENEYETW-----TMGNVNSWNTYVQWKNNGDEKFEQTTPQDFEVLNLT 183
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 180 EPNITLYCVHVESFVPGPPRAQPSKOCARTLKQDS 215
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 184 EFWITTCVQVRGFLPDRNKAQGEWSEPVCEQTHDET 219
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
I10S HUMAN
ID I10S HUMAN STANDARD; PRT; 325 AA.
AC 008334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DT 25-JAN-2005 (Rel. 46, last annotation update)
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE (Cytokine receptor family 2 member 4) (Cytokine receptor class-II
DE CRF2-4).
DE Name=I10RB; Synonyms=CRFB4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=93500510; PubMed=8314576;
RA Lutfalla G., Gardiner K., Uze G.;
RT "A new member of the cytokine receptor gene family maps on chromosome
RT 21 at less than 35 kb from IFNAR.";
RL Genomics 16:356-373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96054036; PubMed=7563119;
RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT "Structure of the human CRFB4 gene: comparison with its IFNAR
RT neighbor.";
RL J. Mol. Evol. 41:338-344(1995).
RN [3]
RP SEQUENCE OF 20-34.
RX PubMed=15340161; DOI=10.1110/pe.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=97459974; PubMed=9312047; DOI=10.1093/emboj/16.19.5894;
RA Pestka S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
RA Pesketa S.;
RT "Identification and functional characterization of a second chain of
RT the interleukin-10 receptor complex.";
RL EMBO J. 16:5894-5903(1997).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=20469498; PubMed=10875937; DOI=10.1074/jbc.M005304200;
RA Xie W.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a novel human cytokine that signals through the
RT interferon receptor-related proteins CRF2-4 and IL-22R.";
RL J. Biol. Chem. 275:31335-31339(2000).
RN [6]
RP FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain
RP essential for the active IL10 receptor complex and to initiate
RP IL10-induced signal transduction events.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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QY 126 L7AP-----EKWKRPEDLPVSMOOIYSNLKYNVSILANTKSNRTWSQCVTNHTLYLTWL 179
Db 131 FLAPKIENEYETW-----TKKNVYNSWTYNNVOYWKNGTDEKFOITPQYDFEVLKRL 181
QY 180 EPNTLYCVHVESFVPGPPRRAPSEKQCARTLKDQS 215
Db 182 EPWTYYCVQVRGFLPDNKKAGWSEPVCEQTTHDET 217

Search completed: February 25, 2005, 02:43:34
Job time : 120.276 secs